

SEQUENCE LISTING

<110> JAPAN SCIENCE AND TECHNOLOGY CORPORATION

<120> Screening of genes to give tolerance against environmental stress and the applications

<130> 12-130

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<150> JP P1999-235910

<151> 1999-07-19

<150> JP P2000-85377

<151> 2000-03-24

<160> 66

<170> PatentIn Ver. 2.1

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<213> Bruguiera sexangula

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Arg Pro Thr Lys Val Gln Glu Leu Cys Val Tyr Glu Met Asn Glu Arg
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Cys Gln Ala Val Ala Asn Ile Val Lys Ser Ser Leu Gly Pro Val Gly  
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Leu Asp Lys Met Leu Val Asp Asp Ile Gly Asp Val Thr Ile Thr Asn  
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Ser Met Lys Val Glu Lys Leu Gly Lys Asp Ser Leu Val Asn Cys Ala	140	145	150	155
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Lys Thr Ser Met Ser Ser Lys Leu Ile Ala Gly Asp Ser Asp Phe Phe	160	165	170	
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Arg Gly Glu Ile Lys Tyr Pro Ile Lys Ser Ile Asn Ile Leu Lys Ala	190	195	200	
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Ser Thr Phe Ala Asp Met Glu Gly Glu Glu Thr Phe Asp Ser Ser Leu	335	340	345	
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gcc ata aca att ctt cga att gat gac atg atc aag ctt gtc aag gat			1697
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Arg Asp Ser Cys Leu Leu Asn Gly Tyr Ala Leu Asn Thr Gly Arg Ala  
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Val Leu Thr Thr Lys Gly Ile Asp Asp Met Ala Leu Lys Tyr Phe Val  
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Glu Ala Gly Ala Ile Ala Val Arg Arg Val Arg Lys Glu Asp Met Arg  
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Glu Val Val Glu Glu Arg Ile Ala Asp Asp Asp Val Ile Met Ile Lys  
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Tyr Pro Asp Met Gly Phe Ala Glu Lys Thr Thr Glu Thr Leu Val  
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ctc ggc gtg ggg cct gag agg gcc cac ttt gag gga gcc gag atg ggc 196  
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gtg ccg gcc gag aac gga ggc tgc aag tgc gga agt aac tgc acc tgc 244  
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Asp Pro Cys Thr Cys Lys  
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Gly Ile Pro Ile Asp Leu Leu Asp Arg Leu Leu Ile Ile Thr Thr Gln	
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Ile Gly Ala Glu Thr Ser Leu Arg Tyr Ala Ile His Leu Ile Thr Ala	
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Ala Ala Leu Ala Cys Gln Lys Arg Lys Gly Lys Leu Val Glu Thr Glu	
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Asp Ile Ser Arg Ala Tyr Asn Leu Phe Leu Asp Val Lys Arg Ser Thr	
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Glu Lys Val Gln Ser Gly Asp Val Ile Ala Ile Asp Lys Ala Ser Gly  
50 55 60  
Lys Ile Thr Lys Leu Gly Arg Ser Phe Ser Arg Ser Arg Asp Tyr Asp  
65 70 75 80  
Ala Met Gly Pro Gln Val Lys Phe Val Gln Cys Pro Asp Gly Glu Leu  
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Gln Lys Arg Lys Glu Val Val His Cys Val Ser Leu His Glu Ile Asp  
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130 135 140  
Ala Glu Trp Arg Glu Glu Gly Lys Ala Glu Ile Val Pro Gly Val Leu  
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Phe Ile Asp Glu Val His Met Leu Asp Ile Glu Cys Phe Ser Phe Leu  
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Gly Ile Pro Ile Asp Leu Leu Asp Arg Leu Leu Ile Ile Thr Thr Gln  
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Pro Tyr Thr Lys Asp Glu Ile Arg Lys Ile Leu Asp Ile Arg Cys Gln  
225 230 235 240

Glu Glu Asp Val Glu Met Ala Glu Glu Ala Lys Ala Leu Leu Thr His  
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Ile Gly Ala Glu Thr Ser Leu Arg Tyr Ala Ile His Leu Ile Thr Ala  
260 265 270

Ala Ala Leu Ala Cys Gln Lys Arg Lys Gly Lys Leu Val Glu Thr Glu  
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His Pro Lys Asn Tyr Gly Pro Gly Ser Arg Ala Cys Arg Val Cys Gly  
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aat ccg cac ggg ttg atc agg aag tac gga ctc atg tgc tgc aga cag 149  
Asn Pro His Gly Leu Ile Arg Lys Tyr Gly Leu Met Cys Cys Arg Gln  
30 35 40

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Cys Phe Arg Ser Asn Ala Lys Glu Ile Gly Phe Ile Lys Tyr Arg  
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Thr Gly His Leu Ile Tyr Lys Leu Gly Gly Ile Asp Lys Arg Val Ile  
25 30 35  
gag agg ttt gag aag gaa gct gct gag atg aac aag agg tca ttc aag 198  
Glu Arg Phe Glu Lys Glu Ala Ala Glu Met Asn Lys Arg Ser Phe Lys  
40 45 50 55  
tat gcc tgg gtg ctt gac aag ctg aag gct gag cgt gag cgt ggt atc 246  
Tyr Ala Trp Val Leu Asp Lys Leu Lys Ala Glu Arg Glu Arg Gly Ile  
60 65 70  
acc att gat att gcc ttg tgg aag ttc gag aca acc aaa tat tac tgc 294  
Thr Ile Asp Ile Ala Leu Trp Lys Phe Glu Thr Thr Lys Tyr Tyr Cys  
75 80 85  
acg gtc att gat gct cct gga cat cgt gac ttt att aag aat atg atc 342  
Thr Val Ile Asp Ala Pro Gly His Arg Asp Phe Ile Lys Asn Met Ile  
90 95 100

acc ggg act tcc caa gct gac tgt gct gtc ctc atc att gac tct acc	390
Thr Gly Thr Ser Gln Ala Asp Cys Ala Val Leu Ile Ile Asp Ser Thr	
105 110 115	
act ggt ggc ttt gag gct ggt atc tct aaa gat ggt cag acc cgc gag	438
Thr Gly Gly Phe Glu Ala Gly Ile Ser Lys Asp Gly Gln Thr Arg Glu	
120 125 130 135	
cat gcc ctg ctt gcc ttc acc ctt ggt gtt aag caa atg att tgc tgc	486
His Ala Leu Leu Ala Phe Thr Leu Gly Val Lys Gln Met Ile Cys Cys	
140 145 150	
tgc aac aag atg gat gct acc act tcc aag tat tct aag gca aga tat	534
Cys Asn Lys Met Asp Ala Thr Thr Ser Lys Tyr Ser Lys Ala Arg Tyr	
155 160 165	
gat gaa att gtt aag gaa gtg tca tcc tac ttg aag aag gtt ggt tac	582
Asp Glu Ile Val Lys Glu Val Ser Ser Tyr Leu Lys Lys Val Gly Tyr	
170 175 180	
aac cca gag aag att cct ttt gtc ccc ata tct gga ttt gag ggt gac	630
Asn Pro Glu Lys Ile Pro Phe Val Pro Ile Ser Gly Phe Glu Gly Asp	
185 190 195	
aac atg att gag aga tcc acc aac ctt gac tgg tac aag ggc cca act	678
Asn Met Ile Glu Arg Ser Thr Asn Leu Asp Trp Tyr Lys Gly Pro Thr	
200 205 210 215	
ctt ctt gag gcc ctg gac atg atc cag gag cca aag agg cca tca gat	726
Leu Leu Glu Ala Leu Asp Met Ile Gln Glu Pro Lys Arg Pro Ser Asp	
220 225 230	
aag ccc ctc cgt ctc cca ctt cag gat gtg tac aag att ggt ggt att	774
Lys Pro Leu Arg Leu Pro Leu Gln Asp Val Tyr Lys Ile Gly Gly Ile	
235 240 245	
ggg aca gtc cca gtg ggt cgt gtt gaa act ggt gtc ctg aag cct gga	822
Gly Thr Val Pro Val Gly Arg Val Glu Thr Gly Val Leu Lys Pro Gly	
250 255 260	
atg gtt gtt act ttt ggt ccc tca gga ctg acc act gaa gtt aag tct	870
Met Val Val Thr Phe Gly Pro Ser Gly Leu Thr Thr Glu Val Lys Ser	
265 270 275	
gtg gag atg cac cat gaa gct ctc caa gag gct ctt ccc gga gac aac	918
Val Glu Met His His Glu Ala Leu Gln Glu Ala Leu Pro Gly Asp Asn	
280 285 290 295	
gtt ggc ttc aat gtt aag aat gtt tcc gtg aag gat ctt aag cgg ggt	966
Val Gly Phe Asn Val Lys Asn Val Ser Val Lys Asp Leu Lys Arg Gly	
300 305 310	
tat gtt gcc tca aac tcc aag gat gat cct gcc aag gag gca tct agc	1014
Tyr Val Ala Ser Asn Ser Lys Asp Asp Pro Ala Lys Glu Ala Ser Ser	
315 320 325	
ttc acc tcc caa gtt atc atc atg aac cac cct ggt cag att gga aat	1062

Phe	Thr	Ser	Gln	Val	Ile	Ile	Met	Asn	His	Pro	Gly	Gln	Ile	Gly	Asn	
330							335						340			
ggt	tat	gcc	cct	gtt	ctg	gat	tgc	cac	acc	tct	cac	att	gct	gtc	aag	1110
Gly	Tyr	Ala	Pro	Val	Leu	Asp	Cys	His	Thr	Ser	His	Ile	Ala	Val	Lys	
345							350					355				
ttt	tct	gag	atc	ctc	aca	aag	att	gat	agg	cga	tct	ggc	aag	gag	ctt	1158
Phe	Ser	Glu	Ile	Leu	Thr	Lys	Ile	Asp	Arg	Arg	Ser	Gly	Lys	Glu	Leu	
360							365				370		375			
gaa	aag	gag	ccc	aag	ttc	ttg	aag	aat	ggt	gat	gct	ggg	ttc	gtg	aag	1206
Glu	Lys	Glu	Pro	Lys	Phe	Leu	Lys	Asn	Gly	Asp	Ala	Gly	Phe	Val	Lys	
							380			385		390				
atg	att	ccg	acc	aag	cct	atg	gtg	gtg	gaa	act	ttc	tcc	gag	tat	cct	1254
Met	Ile	Pro	Thr	Lys	Pro	Met	Val	Val	Glu	Thr	Phe	Ser	Glu	Tyr	Pro	
						395			400		405					
ccg	ctt	ggt	aga	ttt	gcc	gtc	agg	gac	atg	cgc	cag	act	gtt	gca	gtg	1302
Pro	Leu	Gly	Arg	Phe	Ala	Val	Arg	Asp	Met	Arg	Gln	Thr	Val	Ala	Val	
						410			415		420					
gga	gtc	atc	aag	agt	gtc	gag	aaa	aag	gaa	cct	tct	gga	gct	aag	gtg	1350
Gly	Val	Ile	Lys	Ser	Val	Glu	Lys	Glu	Lys	Pro	Ser	Gly	Ala	Lys	Val	
						425			430		435					
act	aaa	tct	gct	gcc	aag	aag	ggt	ggc	aaa	tgaaccgtgc	aagtcaagagt					1400
Thr	Lys	Ser	Ala	Ala	Lys	Lys	Gly	Gly	Lys							
						440			445							
tgatgttagat	gaaggctatt	ggaagaataa	agactgggcc	ctggtagcg	gtctaattat											1460
tggatgttca	gcagttggtt	tcgagaacta	cagttcaat	tcagcgccat	catcacggag											1520
ctgttgttcc	cagaattggg	ttcttgaccg	tcgggtggcat	tggctgttgg	tttgagtgac											1580
ttctttgtgt	catgtttaga	ctttatcgga	tttgctattt	cataaagcgg	cttggaaatt											1640
ttaaaaaaaaaa	aaaaaaaaaa	aaaaaa														1664

<210> 12

<211> 449

<212> PRT

<213> Bruguiera sexangula

<400> 12

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1					5				10			15			

Asp	Ser	Gly	Lys	Ser	Thr	Thr	Gly	His	Leu	Ile	Tyr	Lys	Leu	Gly	
					20				25			30			

Gly	Ile	Asp	Lys	Arg	Val	Ile	Glu	Arg	Phe	Glu	Lys	Glu	Ala	Ala	Glu
					35				40			45			

Met Asn Lys Arg Ser Phe Lys Tyr Ala Trp Val Leu Asp Lys Leu Lys  
50 55 60

Ala Glu Arg Glu Arg Gly Ile Thr Ile Asp Ile Ala Leu Trp Lys Phe  
65 70 75 80

Glu Thr Thr Lys Tyr Tyr Cys Thr Val Ile Asp Ala Pro Gly His Arg  
85 90 95

Asp Phe Ile Lys Asn Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala  
100 105 110

Val Leu Ile Ile Asp Ser Thr Thr Gly Gly Phe Glu Ala Gly Ile Ser  
115 120 125

Lys Asp Gly Gln Thr Arg Glu His Ala Leu Leu Ala Phe Thr Leu Gly  
130 135 140

Val Lys Gln Met Ile Cys Cys Cys Asn Lys Met Asp Ala Thr Thr Ser  
145 150 155 160

Lys Tyr Ser Lys Ala Arg Tyr Asp Glu Ile Val Lys Glu Val Ser Ser  
165 170 175

Tyr Leu Lys Lys Val Gly Tyr Asn Pro Glu Lys Ile Pro Phe Val Pro  
180 185 190

Ile Ser Gly Phe Glu Gly Asp Asn Met Ile Glu Arg Ser Thr Asn Leu  
195 200 205

Asp Trp Tyr Lys Gly Pro Thr Leu Leu Glu Ala Leu Asp Met Ile Gln  
210 215 220

Glu Pro Lys Arg Pro Ser Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp  
225 230 235 240

Val Tyr Lys Ile Gly Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu  
245 250 255

Thr Gly Val Leu Lys Pro Gly Met Val Val Thr Phe Gly Pro Ser Gly  
260 265 270

Leu Thr Thr Glu Val Lys Ser Val Glu Met His His Glu Ala Leu Gln  
275 280 285

Glu Ala Leu Pro Gly Asp Asn Val Gly Phe Asn Val Lys Asn Val Ser  
290 295 300

Val Lys Asp Leu Lys Arg Gly Tyr Val Ala Ser Asn Ser Lys Asp Asp  
305 310 315 320

Pro Ala Lys Glu Ala Ser Ser Phe Thr Ser Gln Val Ile Ile Met Asn  
325 330 335

His Pro Gly Gln Ile Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His  
340 345 350

Thr Ser His Ile Ala Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp  
355 360 365

Arg Arg Ser Gly Lys Glu Leu Glu Lys Glu Pro Lys Phe Leu Lys Asn  
370 375 380

Gly Asp Ala Gly Phe Val Lys Met Ile Pro Thr Lys Pro Met Val Val  
385 390 395 400

Glu Thr Phe Ser Glu Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp  
405 410 415

Met Arg Gln Thr Val Ala Val Gly Val Ile Lys Ser Val Glu Lys Lys  
420 425 430

Glu Pro Ser Gly Ala Lys Val Thr Lys Ser Ala Ala Lys Lys Gly Gly  
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Lys

<210> 13

<211> 770

<212> DNA

<213> Bruguiera sexangula

<220>

<221> CDS

<222> (2)...(769)

<400> 13

c gat gat atg gac gag gcc aca ccc acc ttt gtt tgg ggc acc aat atc 49  
Asp Asp Met Asp Glu Ala Thr Pro Thr Phe Val Trp Gly Thr Asn Ile  
1 5 10 15

agc gtg cag gat gtc aag gcc gct att cag atg ttt ttg aag cac ttc 97  
Ser Val Gln Asp Val Lys Ala Ala Ile Gln Met Phe Leu Lys His Phe  
20 25 30

agg gat agt aat cag agt caa agg aac gag att ttt gaa gaa ggg aag 145  
Arg Asp Ser Asn Gln Ser Gln Arg Asn Glu Ile Phe Glu Glu Gly Lys  
35 40 45

tac gtg aaa gcg ata cat aag gtt ctt gaa gtt gaa gga gag tcg ctt 193  
Tyr Val Lys Ala Ile His Lys Val Leu Glu Val Glu Gly Glu Ser Leu  
50 55 60

gat gtt gat gct cgt gat gtg ttt gat tat gat tct gat ttg tat gcc 241  
Asp Val Asp Ala Arg Asp Val Phe Asp Tyr Asp Ser Asp Leu Tyr Ala  
65 70 75 80

aag atg att cgg tac cca ctt gag gtt ttg gcc att ttc gac att gtt 289  
Lys Met Ile Arg Tyr Pro Leu Glu Val Leu Ala Ile Phe Asp Ile Val  
85 90 95

ttg atg gat att gtg agt ttg atc aac cct ttg ttt gag aaa cat gta	337		
Leu Met Asp Ile Val Ser Leu Ile Asn Pro Leu Phe Glu Lys His Val			
100	105	110	
caa gtc agg att ttc aat ctt aag acc tcg att aca atg aga aat ctc	385		
Gln Val Arg Ile Phe Asn Leu Lys Thr Ser Ile Thr Met Arg Asn Leu			
115	120	125	
aac cct tct gat atc gaa aag atg gtg tca ttg aag gga atg ata att	433		
Asn Pro Ser Asp Ile Glu Lys Met Val Ser Leu Lys Gly Met Ile Ile			
130	135	140	
cgg tgt agt tcc ata ata ccg gag atc agg gaa gca gta ttt aga tgc	481		
Arg Cys Ser Ser Ile Ile Pro Glu Ile Arg Glu Ala Val Phe Arg Cys			
145	150	155	160
ctt gtt tgt ggc tac ttc tct gat ccc atc gtt gtg gat aga gga cgg	529		
Leu Val Cys Gly Tyr Phe Ser Asp Pro Ile Val Val Asp Arg Gly Arg			
165	170	175	
ata agt gaa cct aaa gca tgc ttg aaa gag gaa tgt ctt act aag aac	577		
Ile Ser Glu Pro Lys Ala Cys Leu Lys Glu Glu Cys Leu Thr Lys Asn			
180	185	190	
tcc atg aca cta gtt cac aat cgt tgc agg ttt gct gat aag cag att	625		
Ser Met Thr Leu Val His Asn Arg Cys Arg Phe Ala Asp Lys Gln Ile			
195	200	205	
gtg agg ctc cag gag aca cct gac gag atc cct gaa gga gga aca cca	673		
Val Arg Leu Gln Glu Thr Pro Asp Glu Ile Pro Glu Gly Gly Thr Pro			
210	215	220	
cac acg gtg agc tta ttg atg cat gac aag ctg gta gat gct gga aag	721		
His Thr Val Ser Leu Leu Met His Asp Lys Leu Val Asp Ala Gly Lys			
225	230	235	240
cca ggt gac agg gtt gag gtc act gga att tat agg gct atg agt gtt a	770		
Pro Gly Asp Arg Val Glu Val Thr Gly Ile Tyr Arg Ala Met Ser Val			
245	250	255	
<210> 14			
<211> 256			
<212> PRT			
<213> Bruguiera sexangula			
<400> 14			
Asp Asp Met Asp Glu Ala Thr Pro Thr Phe Val Trp Gly Thr Asn Ile			
1 5 10 15			
Ser Val Gln Asp Val Lys Ala Ala Ile Gln Met Phe Leu Lys His Phe			
20 25 30			
Arg Asp Ser Asn Gln Ser Gln Arg Asn Glu Ile Phe Glu Glu Gly Lys			
35 40 45			
Tyr Val Lys Ala Ile His Lys Val Leu Glu Val Glu Gly Glu Ser Leu			

50	55	60
Asp Val Asp Ala Arg Asp Val Phe Asp Tyr Asp Ser Asp Leu Tyr Ala		
65	70	75
Lys Met Ile Arg Tyr Pro Leu Glu Val Leu Ala Ile Phe Asp Ile Val		
85	90	95
Leu Met Asp Ile Val Ser Leu Ile Asn Pro Leu Phe Glu Lys His Val		
100	105	110
Gln Val Arg Ile Phe Asn Leu Lys Thr Ser Ile Thr Met Arg Asn Leu		
115	120	125
Asn Pro Ser Asp Ile Glu Lys Met Val Ser Leu Lys Gly Met Ile Ile		
130	135	140
Arg Cys Ser Ser Ile Ile Pro Glu Ile Arg Glu Ala Val Phe Arg Cys		
145	150	155
Leu Val Cys Gly Tyr Phe Ser Asp Pro Ile Val Val Asp Arg Gly Arg		
165	170	175
Ile Ser Glu Pro Lys Ala Cys Leu Lys Glu Glu Cys Leu Thr Lys Asn		
180	185	190
Ser Met Thr Leu Val His Asn Arg Cys Arg Phe Ala Asp Lys Gln Ile		
195	200	205
Val Arg Leu Gln Glu Thr Pro Asp Glu Ile Pro Glu Gly Gly Thr Pro		
210	215	220
His Thr Val Ser Leu Leu Met His Asp Lys Leu Val Asp Ala Gly Lys		
225	230	235
240		
Pro Gly Asp Arg Val Glu Val Thr Gly Ile Tyr Arg Ala Met Ser Val		
245	250	255

<210> 15  
<211> 846  
<212> DNA  
<213> *Mesembryanthemum crystallinum*

<220>  
<221> CDS  
<222> (39)..(530)

<400> 15  
caaattttct ttgctgaatc gaatctacaa aataccctg atg ggt cag gtt ctt gac 56  
Met Gly Gln Val Leu Asp  
1 5

aaa ttt caa cgt aag caa tgg aga caa aag caa atc cag aag ata aca 104  
Lys Phe Gln Arg Lys Gln Trp Arg Gln Lys Gln Ile Gln Lys Ile Thr  
10 15 20

gat aag gta ttt gat cgt gtc aaa agt ccg acc gga aat ggc act ctt	152		
Asp Lys Val Phe Asp Arg Val Lys Ser Pro Thr Gly Asn Gly Thr Leu			
25	30	35	
aca ttt gaa gag ctg tat ata gct acc ctg att gtc tac aat gat ata	200		
Thr Phe Glu Glu Leu Tyr Ile Ala Thr Leu Ile Val Tyr Asn Asp Ile			
40	45	50	
aac aag tat ttg ccg ggg ccg cac ttt gat cct cca tcg aaa gac aaa	248		
Asn Lys Tyr Leu Pro Gly Pro His Phe Asp Pro Ser Lys Asp Lys			
55	60	65	70
atc aga gcc ttg atg cag gaa tgc gat atg gat gtc gat gga gaa ctt	296		
Ile Arg Ala Leu Met Gln Glu Cys Asp Met Asp Val Asp Gly Glu Leu			
75	80	85	
aac cgt gag gaa ttt gtg aag ttc atg cag aag gtg aca gcc gat aca	344		
Asn Arg Glu Glu Phe Val Lys Phe Met Gln Lys Val Thr Ala Asp Thr			
90	95	100	
ttc tct acg gtc agc cag gga ctg att atc tct ctg att ctg gcg cca	392		
Phe Ser Thr Val Ser Gln Gly Leu Ile Ile Ser Leu Ile Leu Ala Pro			
105	110	115	
aca gtt gca ttg gcg acg aag agg gca aca gaa ggt gtt cca ggt gtg	440		
Thr Val Ala Leu Ala Thr Lys Arg Ala Thr Glu Gly Val Pro Gly Val			
120	125	130	
ggg aaa gtg gtg caa aag gtg cct act tca att tat gca tcc ctg gtg	488		
Gly Lys Val Val Gln Lys Val Pro Thr Ser Ile Tyr Ala Ser Leu Val			
135	140	145	150
acc ctt gtt gtc gtt gca atc caa act gct agc gag gga tgc	530		
Thr Leu Val Val Ala Ile Gln Thr Ala Ser Glu Gly Cys			
155	160		
tgattagagg cttagttac ttgttcatga tacagaagga acagtcttgg tcaatttatt	590		
tctttttaa taggacataa ggaagttgta tatcttctt cttcttcta ccaggtttg	650		
gggaaagttg gaaagaacat acaaatgatt tcaactgcgt attggctgat cctccat	710		
ataaaaactt gtcgtgtcta gcatgagcga ttcaatattt gcaatatgca atatttgta	770		
tgtatgtctac attcagtgat tagtgtgatt gtgcagtttggggaaaaaaa aaaaaaaaaa	830		
aaaaaaaaaaaa aaaaaaa	846		

<210> 16  
 <211> 164  
 <212> PRT  
 <213> *Mesembryanthemum crystallinum*

<400> 16  
 Met Gly Gln Val Leu Asp Lys Phe Gln Arg Lys Gln Trp Arg Gln Lys

1	5	10	15
Gln Ile Gln Lys Ile Thr Asp Lys Val Phe Asp Arg Val Lys Ser Pro			
20	25		30
Thr Gly Asn Gly Thr Leu Thr Phe Glu Glu Leu Tyr Ile Ala Thr Leu			
35	40		45
Ile Val Tyr Asn Asp Ile Asn Lys Tyr Leu Pro Gly Pro His Phe Asp			
50	55		60
Pro Pro Ser Lys Asp Lys Ile Arg Ala Leu Met Gln Glu Cys Asp Met			
65	70		75
			80
Asp Val Asp Gly Glu Leu Asn Arg Glu Glu Phe Val Lys Phe Met Gln			
85		90	
			95
Lys Val Thr Ala Asp Thr Phe Ser Thr Val Ser Gln Gly Leu Ile Ile			
100		105	
			110
Ser Leu Ile Leu Ala Pro Thr Val Ala Leu Ala Thr Lys Arg Ala Thr			
115		120	
			125
Glu Gly Val Pro-Gly Val Gly Lys Val Val Gln Lys Val Pro Thr Ser			
130	135		140
Ile Tyr Ala Ser Leu Val Thr Leu Val Val Val Ala Ile Gln Thr Ala			
145	150		155
			160
Ser Glu Gly Cys			

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<210> 17
<211> 872
<212> DNA
<213> Mesembryanthemum crystallinum

<220>
<221> CDS
<222> (183)..(569)

<400> 17
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agtaagctct gtcctttgc tctctgttga atgtactatc ttctgtgaac caaaggccaa 120
agattaacta ttggagattt ctctactcga aatttgtttt taggtgttga ccctgtttag 180
ct atg gcg aac aag ccc caa att cca acg aag aat tcg gcc ctc att 227
  Met Ala Asn Lys Pro Gln Ile Pro Thr Lys Asn Ser Ala Leu Ile
   1           5           10          15
gct att atc gcg gat gag gat act gta act gga ttt ttg ctg gct gga 275
  Ala Ile Ile Ala Asp Glu Asp Thr Val Thr Gly Phe Leu Leu Ala Gly
   20          25          30
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gtt ggt aat gtt gat cta cga aga cag aca aat tac att att gtg gac	323		
Val Gly Asn Val Asp Leu Arg Arg Gln Thr Asn Tyr Ile Ile Val Asp			
35	40	45	
aat aaa aca acg atg aag caa atc gaa gat gca ttc aag gag ttc aca	371		
Asn Lys Thr Thr Met Lys Gln Ile Glu Asp Ala Phe Lys Glu Phe Thr			
50	55	60	
gca aga gag gac att gcg gtt gta cta atc agc caa tat gtt gca aat	419		
Ala Arg Glu Asp Ile Ala Val Val Leu Ile Ser Gln Tyr Val Ala Asn			
65	70	75	
atg ata aga gta ttg gtt gat agc tac aac aaa cca atc ccg gca att	467		
Met Ile Arg Val Leu Val Asp Ser Tyr Asn Lys Pro Ile Pro Ala Ile			
80	85	90	95
ttg gag att cct tca aag gac cat cct tat gat cct aac cat gat tca	515		
Leu Glu Ile Pro Ser Lys Asp His Pro Tyr Asp Pro Asn His Asp Ser			
100	105	110	
gtc ctt tca agg gtt aaa tac ctg ttc tct tct gaa tcg gca tca agc	563		
Val Leu Ser Arg Val Lys Tyr Leu Phe Ser Ser Glu Ser Ala Ser Ser			
115	120	125	
aga ttt tagccatatg ctttgtaaag ttccctgctc ctgaatgttt ggtgattatg	619		
Arg Phe			
agtttaaact agaaccagtc acattctgac ttggatattt gaggcactgt ttgtttatg	679		
ttcttaaaat aaggagtgtt attacgactc catgaatcg gatatgactc catgaatcgc	739		
atgtatttct ttccatctca tttgaaagag tcgagcagcc atatcatttta gtttcttct	799		
cttgcgaatg agcttggaaag aaatgtttt gctataaaag atttcaactc ttggtaaaaa	859		
aaaaaaaaaaa aaa	872		

<210> 18  
<211> 129  
<212> PRT  
<213> *Mesembryanthemum crystallinum*

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<400> 18
Met Ala Asn Lys Pro Gln Ile Pro Thr Lys Asn Ser Ala Leu Ile Ala
  1           5           10          15

Ile Ile Ala Asp Glu Asp Thr Val Thr Gly Phe Leu Leu Ala Gly Val
  20          25          30

Gly Asn Val Asp Leu Arg Arg Gln Thr Asn Tyr Ile Ile Val Asp Asn
  35          40          45

Lys Thr Thr Met Lys Gln Ile Glu Asp Ala Phe Lys Glu Phe Thr Ala
  50          55          60

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Arg Glu Asp Ile Ala Val Val Leu Ile Ser Gln Tyr Val Ala Asn Met  
65 70 75 80

Ile Arg Val Leu Val Asp Ser Tyr Asn Lys Pro Ile Pro Ala Ile Leu  
85 90 95

Glu Ile Pro Ser Lys Asp His Pro Tyr Asp Pro Asn His Asp Ser Val  
100 105 110

Leu Ser Arg Val Lys Tyr Leu Phe Ser Ser Glu Ser Ala Ser Ser Arg  
115 120 125

Phe

<210> 19

<211> 647

<212> DNA

<213> *Mesembryanthemum crystallinum*

<220>

<221> CDS

<222> (64)..(426)

<400> 19

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Met Ala Tyr Ala Met Lys Pro Thr Lys Pro Gly Met Glu Glu Ser  
1 5 10 15

cag gag cag att cac aag atc agg atc act ctt tct tct aag aac gtc 156  
Gln Glu Gln Ile His Lys Ile Arg Ile Thr Leu Ser Ser Lys Asn Val  
20 25 30

aag aac ctt gag aaa gtg tgt gct gat ctt gta cgc ggt gca aag gac 204  
Lys Asn Leu Glu Lys Val Cys Ala Asp Leu Val Arg Gly Ala Lys Asp  
35 40 45

aag cgc ctc agg gtt aag gga cca gtg agg atg ccc acc aag gtt ctg 252  
Lys Arg Leu Arg Val Lys Gly Pro Val Arg Met Pro Thr Lys Val Leu  
50 55 60

aag atc aca aca agg aag tct ccc tgt ggt gaa gga acc aac acc ttt 300  
Lys Ile Thr Thr Arg Lys Ser Pro Cys Gly Glu Gly Thr Asn Thr Phe  
65 70 75

gac aga ttt gag ttg cgt gtt cac aag aga gtc att gac ctc ttc agc 348  
Asp Arg Phe Glu Leu Arg Val His Lys Arg Val Ile Asp Leu Phe Ser  
80 85 90 95

tcc cca gac gtg gtc aag cag atc acc tcc atc acc att gaa cct ggt 396  
Ser Pro Asp Val Val Lys Gln Ile Thr Ser Ile Thr Ile Glu Pro Gly  
100 105 110

gtt gag gtt gag gtt aca ata gct gac tct tagacatgcc tggtgaagtt 446  
Val Glu Val Glu Val Val Thr Ile Ala Asp Ser  
115 120

gtcgtcgttg tagggctgtt gtagctgtct catatagtgg tgctatctca ctaagaattt 506  
tgaagatact aaattgtttg tttgaaagag atgtttctt tagctgtaat gttatgtttt 566  
tgaaggtgtt ggaacatgca ttatgttata atgctttatc aatagaactt ccaatttgaa 626  
tgcaaaaaaaaaaaaaaaa a 647

<210> 20  
<211> 121  
<212> PRT  
<213> *Mesembryanthemum crystallinum*

<400> 20  
Met Ala Tyr Ala Met Lys Pro Thr Lys Pro Gly Met Glu Glu Ser Gln  
1 5 10 15

Glu Gln Ile His Lys Ile Arg Ile Thr Leu Ser Ser Lys Asn Val Lys  
20 25 30

Asn Leu Glu Lys Val Cys Ala Asp Leu Val Arg Gly Ala Lys Asp Lys  
35 40 45

Arg Leu Arg Val Lys Gly Pro Val Arg Met Pro Thr Lys Val Leu Lys  
50 55 60

Ile Thr Thr Arg Lys Ser Pro Cys Gly Glu Gly Thr Asn Thr Phe Asp  
65 70 75 80

Arg Phe Glu Leu Arg Val His Lys Arg Val Ile Asp Leu Phe Ser Ser  
85 90 95

Pro Asp Val Val Lys Gln Ile Thr Ser Ile Thr Ile Glu Pro Gly Val  
100 105 110

Glu Val Glu Val Thr Ile Ala Asp Ser  
115 120

<210> 21  
<211> 686  
<212> DNA  
<213> *Sueada japonica*

<220>  
<221> CDS  
<222> (62)..(493)

<400> 21  
acaccattca caaaaacacat taaaaaaaaa cactacttct ttctttctta gccacttgaa 60

a atg gcc tac tca aag gct gta ctc ctt gcc ctt atc ttt gct gtg act 109  
 Met Ala Tyr Ser Lys Ala Val Leu Leu Ala Leu Ile Phe Ala Val Thr  
 1 5 10 15

ctt gtc att gcc tct cag gtc tca gct cgt gaa ctt gct gag gag aca 157  
 Leu Val Ile Ala Ser Gln Val Ser Ala Arg Glu Leu Ala Glu Glu Thr  
 20 25 30

caa tct gtg gag gag tct aag gga tac ggt ggt ggg cac gga ggt cac 205  
 Gln Ser Val Glu Glu Ser Lys Gly Tyr Gly Gly His Gly Gly His  
 35 40 45

tat ggt ggt ggt cac tat ggt ggt gga cac aga cac ggt ggc cat gga 253  
 Tyr Gly Gly His Tyr Gly Gly His Arg His Gly Gly His Gly  
 50 55 60

cac tac gca act gag gaa gca gag aac aag aat gaa gcc gta gaa cct 301  
 His Tyr Ala Thr Glu Glu Ala Glu Asn Lys Asn Glu Ala Val Glu Pro  
 65 70 75 80

caa ggc ggc tat ggt cac gga cac gga gga ggc tac gga cac ggt ggt 349  
 Gln Gly Gly Tyr Gly His Gly His Gly Gly Tyr Gly His Gly Gly  
 85 90 95

ggc tac gga cac ggt gga ggc tac gga cac gga ggt ggc tac ggg cac 397  
 Gly Tyr Gly His Gly Gly Tyr Gly His Gly Gly Tyr Gly His Gly  
 100 105 110

ggt ggt ggc tac gga cat gga ggt ggt tat gga cac ggt gga cac ggt 445  
 Gly Gly Tyr Gly His Gly Gly Tyr Gly His Gly Gly His Gly  
 115 120 125

gga cat ggt ggt cat ggt cac tac gcc aag act acc gag gaa caa aat 493  
 Gly His Gly His Gly His Tyr Ala Lys Thr Thr Glu Glu Gln Asn  
 130 135 140

taagttatgg gttactaaaa cttaaattgt acgttgtcaa ataaaaatgta ctttatgatt 553  
 ttacatgagt atgcatgtaa ttcatcataa gcttcaagga ctatcttgta ctctatgtta 613  
 tataacctata tgaaatggaa gcgtgacttt tattactgta aaaaaaaaaa aaaaaaaaaa 673  
 aaaaaaaaaa aaa 686

<210> 22  
 <211> 144  
 <212> PRT  
 <213> Sueada japonica

<400> 22  
 Met Ala Tyr Ser Lys Ala Val Leu Leu Ala Leu Ile Phe Ala Val Thr  
 1 5 10 15

Leu Val Ile Ala Ser Gln Val Ser Ala Arg Glu Leu Ala Glu Glu Thr  
 20 25 30

35	40	45
Tyr Gly Gly Gly His Tyr Gly Gly His Arg His Gly Gly His Gly		
50	55	60
His Tyr Ala Thr Glu Glu Ala Glu Asn Lys Asn Glu Ala Val Glu Pro		
65	70	75
Gln Gly Gly Tyr Gly His Gly His Gly Gly Tyr Gly His Gly Gly		
85	90	95
Gly Tyr Gly His Gly Gly Tyr Gly His Gly Gly Tyr Gly His		
100	105	110
Gly Gly Gly Tyr Gly His Gly Gly Tyr Gly His Gly Gly His Gly		
115	120	125
Gly His Gly Gly His Gly His Tyr Ala Lys Thr Thr Glu Glu Gln Asn		
130	135	140

<210> 23  
 <211> 683  
 <212> DNA  
 <213> Salsola komarovii

<220>  
 <221> CDS  
 <222> (48)..(362)

<400> 23  
 gttaagatat tatattgcaa ctttacaaag catttctgca actaaat atg gcc ttt 56  
 Met Ala Phe  
 1

tcc aaa cct cta att gct tct cta ctt ctt tct ctc ttt gtt ctt cag 104  
 Ser Lys Pro Leu Ile Ala Ser Leu Leu Leu Ser Leu Phe Val Leu Gln  
 5 10 15

ttt gtt cat gca gtt gaa cct att tca tcc tcc aat caa gtg ggt agc 152  
 Phe Val His Ala Val Glu Pro Ile Ser Ser Asn Gln Val Gly Ser  
 20 25 30 35

aac act gga ggt acc tca gag agt aaa gtg gat tgt ggg gcg gca tgt 200  
 Asn Thr Gly Thr Ser Glu Ser Lys Val Asp Cys Gly Ala Ala Cys  
 40 45 50

acg gtg agg tgc agc gcc tcg aag agg cca aac cta tgc aac agg tca 248  
 Thr Val Arg Cys Ser Ala Ser Lys Arg Pro Asn Leu Cys Asn Arg Ser  
 55 60 65

tgt ggc agt tgt tgc aag acg tgc aac tgc gtg cca cca ggc act tcc 296  
 Cys Gly Ser Cys Cys Lys Thr Cys Asn Cys Val Pro Pro Gly Thr Ser  
 70 75 80

ggc aac tac gaa gcc tgc cct tgt tac gcc aac ttg acc acc cac ggc 344

Gln Ser Val Glu Glu Ser Lys Gly Tyr Gly Gly His Gly Gly His

, P□^, X, P

Gly Asn Tyr Glu Ala Cys Pro Cys Tyr Ala Asn Leu Thr Thr His Gly		
85	90	95
aat cga cac aag tgc cct taattaacaa gaattgttta gttgtttatt		392
Asn Arg His Lys Cys Pro		
100	105	
acatccgtac catgtaacgt actcctattt acactactag agtactagta ataaacattt	452	
ttaggcacgg tccagttgtt catgtagcta gtggtatatt gagtcataaa tgagtgattg	512	
aaaatgagat atgataaaag tgtattatct acattgttagt actgtttgt atcatagtgt	572	
agtgatgttt attttcgta ccttaattt gttactttgt attcccttgc attctatcta	632	
tttacaatcc ttttgtaagt ttatgtaaa aaaaaaaaaa aaaaaaaaaa a	683	

<210> 24  
<211> 105  
<212> PRT  
<213> Salsola komarovii

<400> 24			
Met Ala Phe Ser Lys Pro Leu Ile Ala Ser Leu Leu Ser Leu Phe			
1	5	10	15

Val Leu Gln Phe Val His Ala Val Glu Pro Ile Ser Ser Ser Asn Gln		
20	25	30

Val Gly Ser Asn Thr Gly Gly Thr Ser Glu Ser Lys Val Asp Cys Gly		
35	40	45

Ala Ala Cys Thr Val Arg Cys Ser Ala Ser Lys Arg Pro Asn Leu Cys		
50	55	60

Asn Arg Ser Cys Gly Ser Cys Cys Lys Thr Cys Asn Cys Val Pro Pro			
65	70	75	80

Gly Thr Ser Gly Asn Tyr Glu Ala Cys Pro Cys Tyr Ala Asn Leu Thr		
85	90	95

Thr His Gly Asn Arg His Lys Cys Pro		
100	105	

<210> 25  
<211> 803  
<212> DNA  
<213> Salsola komarovii

<220>  
<221> CDS  
<222> (51)..(593)

<400> 25



<210> 26  
<211> 181  
<212> PRT  
<213> Salsola komarovii

<400> 26  
Met Gly Leu Ser Phe Thr Lys Leu Phe Ser Arg Leu Phe Ala Lys Lys  
1 5 10 15  
  
Glu Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr  
20 25 30  
  
Ile Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr  
35 40 45  
  
Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr  
50 55 60  
  
Val Trp Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His  
65 70 75 80  
  
Tyr Phe Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp  
85 90 95  
  
Arg Asp Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn  
100 105 110  
  
Glu Asp Glu Leu Arg Asp Ala Val Leu Leu Val Phe Ala Asn Lys Gln  
115 120 125  
  
Asp Leu Pro Asn Ala Met Asn Ala Ala Glu Ile Thr Asp Lys Leu Gly  
130 135 140  
  
Leu His Ser Leu Arg Gln Arg His Trp Tyr Ile Gln Ser Thr Cys Ala  
145 150 155 160  
  
Thr Ser Gly Glu Gly Leu Tyr Glu Gly Leu Asp Trp Leu Ser Asn Asn  
165 170 175  
  
Ile Ala Ser Lys Ala  
180

<210> 27  
<211> 680  
<212> DNA  
<213> Avicennia marina  
  
<220>  
<221> CDS  
<222> (161) .. (454)

<400> 27  
ctaaaagcca aaggcaagat aagaaacagg ttcctttagc tatcttcctc gtctcgctgc 60

tgcaaaagtt	ccatccccag	aagatcagga	aaacccttct	gcagcagcac	tctaataatc	120										
ctccaatttt	gattcaagag	aagaaacaaa	ataaacagaa	atg	gct	cgc	tct	ttc	175							
				Met	Ala	Arg	Ser	Phe								
				1				5								
tcc	aac	gct	aag	acc	gtc	tct	gtc	att	gcc	aac	gaa	atc	tca	gct	223	
Ser	Asn	Ala	Lys	Thr	Val	Ser	Ala	Val	Ile	Ala	Asn	Glu	Ile	Ser	Ala	
				10				15				20				
ctt	gtc	acc	agg	agg	ggt	tat	gct	gtc	ctc	gca	cag	ggc	gtt	gtt	tcg	271
Leu	Val	Thr	Arg	Arg	Gly	Tyr	Ala	Ala	Leu	Ala	Gln	Gly	Val	Val	Ser	
				25				30				35				
agc	agc	gcg	aga	agc	ggc	ggc	gct	ccg	aac	gtg	atg	ctg	aag	aaa	gga	319
Ser	Ser	Ala	Arg	Ser	Gly	Gly	Ala	Pro	Asn	Val	Met	Leu	Lys	Lys	Gly	
				40				45				50				
tcc	gaa	gaa	tcc	ggg	aag	aca	gca	tgg	gtg	ccc	gac	ccg	gac	acc	ggc	367
Ser	Glu	Glu	Ser	Gly	Lys	Thr	Ala	Trp	Val	Pro	Asp	Pro	Asp	Thr	Gly	
				55				60				65				
tac	tac	cga	ccg	gga	aac	gag	gac	aag	gcc	gcg	ctg	gac	ccg	gtc	gag	415
Tyr	Tyr	Arg	Pro	Gly	Asn	Glu	Asp	Lys	Ala	Ala	Leu	Asp	Pro	Val	Glu	
				70				75				80			85	
ctg	cgg	gag	atg	ctc	atc	aag	aac	aag	ccc	agc	cga	caa	tgaatgaacc		464	
Leu	Arg	Glu	Met	Leu	Ile	Lys	Asn	Lys	Pro	Ser	Arg	Gln				
				90				95								
aagaattgtg	ggattctcat	taattcctcc	cctgttctgg	tccatcgctcg	gaatctgaac	524										
ctgttgttcg	tctagaaatt	cgttcccatg	gaaatctatc	aaagtctgtt	ttcttgccat	584										
ggctcttcct	gtcccatata	tgtatgtcct	caggtgtggc	ctggggtggt	ttgatagata	644										
tataaaatgt	ggtgaattta	aaaaaaaaaa	aaaaaaa			680										

<210> 28  
 <211> 98  
 <212> PRT  
 <213> Avicennia marina

<400> 28																
Met	Ala	Arg	Ser	Phe	Ser	Asn	Ala	Lys	Thr	Val	Ser	Ala	Val	Ile	Ala	
1				5					10				15			
Asn	Glu	Ile	Ser	Ala	Leu	Val	Thr	Arg	Arg	Gly	Tyr	Ala	Ala	Leu	Ala	
				20				25				30				
Gln	Gly	Val	Val	Ser	Ser	Ser	Ala	Arg	Ser	Gly	Gly	Ala	Pro	Asn	Val	
				35				40				45				
Met	Leu	Lys	Lys	Gly	Ser	Glu	Glu	Ser	Gly	Lys	Thr	Ala	Trp	Val	Pro	
				50				55				60				

Asp Pro Asp Thr Gly Tyr Tyr Arg Pro Gly Asn Glu Asp Lys Ala Ala  
65 70 75 80

Leu Asp Pro Val Glu Leu Arg Glu Met Leu Ile Lys Asn Lys Pro Ser  
85 90 95

Arg Gln

<210> 29

<211> 490

<212> DNA

<213> Avicennia marina

<220>

<221> CDS

<222> (20)..(349)

<400> 29

tcggctgggc aaagaaggg atg gcg att cca tcg gaa att cgg gac ttt att 52  
Met Ala Ile Pro Ser Glu Ile Arg Asp Phe Ile  
1 5 10

gct agc cgc aac aga tct ttg gtg atc gca tct cca aag gaa gat gag 100  
Ala Ser Arg Asn Arg Ser Leu Val Ile Ala Ser Pro Lys Glu Asp Glu  
15 20 25

aaa att ctc cgc tca agg cag tgc acc gaa gaa ggg gcg cgt gca gga 148  
Lys Ile Leu Arg Ser Arg Gln Cys Thr Glu Glu Gly Ala Arg Ala Gly  
30 35 40

gcc aaa gct gct gca gtt gct tgc gtt gcc agc gcc att ccc act ctg 196  
Ala Lys Ala Ala Ala Val Ala Cys Val Ala Ser Ala Ile Pro Thr Leu  
45 50 55

gta gct gtt cga acg att ccg tgg gca aag gca aac ctc aac tat aca 244  
Val Ala Val Arg Thr Ile Pro Trp Ala Lys Ala Asn Leu Asn Tyr Thr  
60 65 70 75

gcc cag gca ctc att ata tct tct gca tcc ata gcg gca tac ttt atc 292  
Ala Gln Ala Leu Ile Ile Ser Ser Ala Ser Ile Ala Ala Tyr Phe Ile  
80 85 90

gct gct gac aaa acc atc tta gag tgc gca cgg aaa aat gca gag tac 340  
Ala Ala Asp Lys Thr Ile Leu Glu Cys Ala Arg Lys Asn Ala Glu Tyr  
95 100 105

aaa tcg gct taagatgtatg tgtaagacaa tgtgctcagc ttgcaatgct 389  
Lys Ser Ala  
110

tgccatgact tgtgtttatg tgtatccaa gtttctgaaa ctagcatttt gattttgtgt 449

tccaatgcaa tgagcattat ggaaaaaaaa aaaaaaaaaa a 490

<210> 30  
<211> 110  
<212> PRT  
<213> Avicennia marina

<400> 30  
Met Ala Ile Pro Ser Glu Ile Arg Asp Phe Ile Ala Ser Arg Asn Arg  
1 5 10 15  
Ser Leu Val Ile Ala Ser Pro Lys Glu Asp Glu Lys Ile Leu Arg Ser  
20 25 30  
Arg Gln Cys Thr Glu Glu Gly Ala Arg Ala Gly Ala Lys Ala Ala Ala  
35 40 45  
Val Ala Cys Val Ala Ser Ala Ile Pro Thr Leu Val Ala Val Arg Thr  
50 55 60  
Ile Pro Trp Ala Lys Ala Asn Leu Asn Tyr Thr Ala Gln Ala Leu Ile  
65 70 75 80  
Ile Ser Ser Ala Ser Ile Ala Ala Tyr Phe Ile Ala Ala Asp Lys Thr  
85 90 95  
Ile Leu Glu Cys Ala Arg Lys Asn Ala Glu Tyr Lys Ser Ala  
100 105 110

<210> 31  
<211> 592  
<212> DNA  
<213> Avicennia marina

<220>  
<221> CDS  
<222> (75)..(320)

<400> 31  
gcagtctcag ctttcctgct ctcctgggtgc cttcaaattt gtgaatttct cgagtgctaa 60  
aagattcagc caag atg cag aac gaa gag ggg caa aac atg gat ctc tac 110  
Met Gln Asn Glu Gly Gln Asn Met Asp Leu Tyr  
1 5 10  
atc ccc agg aaa tgc tct gcc acg aac agg ctg atc acc tcc aag gat 158  
Ile Pro Arg Lys Cys Ser Ala Thr Asn Arg Leu Ile Thr Ser Lys Asp  
15 20 25  
cat gct tct gtc cag atc aat gtt ggg cac ttg gat gag aat ggc cga 206  
His Ala Ser Val Gln Ile Asn Val Gly His Leu Asp Glu Asn Gly Arg  
30 35 40  
tac act ggc caa tac tct acc ttt gct ctt tgt gga ttc atc cgt gct 254  
Tyr Thr Gly Gln Tyr Ser Thr Phe Ala Leu Cys Gly Phe Ile Arg Ala

45	50	55	60	
cag ggt gat gct gac agt gct ctt gat agg ctc tgg cag aaa aag aaa				302
Gln Gly Asp Ala Asp Ser Ala Leu Asp Arg Leu Trp Gln Lys Lys Lys				
65	70	75		
gtc gaa acc agg cag cag tgatcctgct caattcagca gtgaaagttt				350
Val Glu Thr Arg Gln Gln				
80				
tttgggtttt gttctgtgtt gtgttattta tgctttcca gaatcaattt ctgtactgga				410
ttgagtatta aaaatgtgga gctaaagggtt gggagacctg atgcctttgt tactcgagta				470
atcacaagta gatactggc ttgtaatagc gtgataattt tgccctgctc ttgcctcatt				530
gactacgaat cagttatgtt attagacaat gttaatctcc aaaaaaaaaa aaaaaaaaaa				590
aa				592

<210> 32  
<211> 82  
<212> PRT  
<213> Avicennia marina

<400> 32				
Met Gln Asn Glu Glu Gly Gln Asn Met Asp Leu Tyr Ile Pro Arg Lys				
1	5	10	15	
Cys Ser Ala Thr Asn Arg Leu Ile Thr Ser Lys Asp His Ala Ser Val				
20	25	30		
Gln Ile Asn Val Gly His Leu Asp Glu Asn Gly Arg Tyr Thr Gly Gln				
35	40	45		
Tyr Ser Thr Phe Ala Leu Cys Gly Phe Ile Arg Ala Gln Gly Asp Ala				
50	55	60		
Asp Ser Ala Leu Asp Arg Leu Trp Gln Lys Lys Lys Val Glu Thr Arg				
65	70	75	80	
Gln Gln				

<210> 33  
<211> 1806  
<212> DNA  
<213> Avicennia marina

<220>  
<221> CDS  
<222> (362)..(1552)

<400> 33

tgtgaaggta aagtctacag catatttcgc gccgctcggt tgattacgtg ttgctttat 60  
 ttggaattt gatagcgctg agtagccgat gccgctggag ggtattgtt attttaggaa 120  
 tacgggtttg tttgattcgc agtttactg tctctagggt tggccctga ggcttctgg 180  
 atttggatt taatcgctga tcgaacagtt tcctggagaa aataactccta gtgcgcata 240  
 atctgatttgc tgacgagaa attgatacac gttatgcga ttgagtttgc tttgcgc 300  
 agataactccg agtgctcgct agatgtggat aatccggagg gctgtttcga tgagatgagg 360  
 g atg tta tca ggg tta atg aac ttc ctg tgg gcc tgg ttt cgg cca agg 409  
     Met Leu Ser Gly Leu Met Asn Phe Leu Trp Ala Cys Phe Arg Pro Arg  
     1                   5                   10                   15  
  
 gcg gat cga agt gtt cac acg ggt tca gat gca ggc ggt cgt cag gat 457  
   Ala Asp Arg Ser Val His Thr Gly Ser Asp Ala Gly Gly Arg Gln Asp  
   20                   25                   30  
  
 ggg ctt tta tgg tat aag gac ttg ggg caa cat atc aat gga gag ttt 505  
   Gly Leu Leu Trp Tyr Lys Asp Leu Gly Gln His Ile Asn Gly Glu Phe  
   35                   40                   45  
  
 tca atg gct gta gtt caa gca aat aac tta cta gag gat cag agt caa 553  
   Ser Met Ala Val Val Gln Ala Asn Asn Leu Leu Glu Asp Gln Ser Gln  
   50                   55                   60  
  
 ctt gaa tct ggt tgc ctg agc ttg agt gat tca gga caa tat ggc act 601  
   Leu Glu Ser Gly Cys Leu Ser Leu Ser Asp Ser Gly Gln Tyr Gly Thr  
   65                   70                   75                   80  
  
 ttt gtg ggg att tat gat gga cat gga ggt cct gag acc tct cgg ttt 649  
   Phe Val Gly Ile Tyr Asp Gly His Gly Gly Pro Glu Thr Ser Arg Phe  
   85                   90                   95  
  
 atc aat gac cat ctc ttc caa cat ata aag aga ttc aca gct gag cat 697  
   Ile Asn Asp His Leu Phe Gln His Ile Lys Arg Phe Thr Ala Glu His  
   100                105                110  
  
 caa tca atg tca gct gag gtc att cac aag gcc att caa gcg act gaa 745  
   Gln Ser Met Ser Ala Glu Val Ile His Lys Ala Ile Gln Ala Thr Glu  
   115                120                125  
  
 gaa ggt ttt ttc tcg gtt agc aga caa tgg tcc atg caa cca cag 793  
   Glu Gly Phe Phe Ser Val Val Ser Arg Gln Trp Ser Met Gln Pro Gln  
   130                135                140  
  
 att gca gca gtt ggc tct tgc tgc ctt gtt ggt gtc atc tgg agt ggc 841  
   Ile Ala Ala Val Gly Ser Cys Cys Leu Val Gly Val Ile Cys Ser Gly  
   145                150                155                160  
  
 act ctt tat gtt tcc aac ctt ggt gat tcc cgt gct gtt ctt ggg acg 889  
   Thr Leu Tyr Val Ser Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Thr  
   165                170                175  
  
 ctt tcc aag gct aca ggg gaa gta cag gct act caa ctc tca aca gag 937

Leu Ser Lys Ala Thr Gly Glu Val Gln Ala Thr Gln Leu Ser Thr Glu			
180	185	190	
cat aat gca agt ttt gag tct gtg aga cgg gaa ctg cag tct ctg cac			985
His Asn Ala Ser Phe Glu Ser Val Arg Arg Glu Leu Gln Ser Leu His			
195	200	205	
cca gat gac tca cag att gtg gtt cta aag cat aat gta tgg cga gtg			1033
Pro Asp Asp Ser Gln Ile Val Val Leu Lys His Asn Val Trp Arg Val			
210	215	220	
aag ggt ctt ata cag atc tca aga tca att gga gat gtg tat ttg aaa			1081
Lys Gly Leu Ile Gln Ile Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys			
225	230	235	240
aag gct gaa ttc aac agg gag cct cta tat cag aaa ttt cga ctt cgt			1129
Lys Ala Glu Phe Asn Arg Glu Pro Leu Tyr Gln Lys Phe Arg Leu Arg			
245	250	255	
gaa gct ttc aaa aga cca att ttg agc tca gaa cca gaa act act gtg			1177
Glu Ala Phe Lys Arg Pro Ile Leu Ser Ser Glu Pro Glu Thr Thr Val			
260	265	270	
cac cag ctg ctg cct cat gat caa ttc att atc ttc gca tca gat ggc			1225
His Gln Leu Leu Pro His Asp Gln Phe Ile Ile Phe Ala Ser Asp Gly			
275	280	285	
ctt tgg gag cac ctt tcc aac caa gaa gca gtt gat ctt gtt cag aaa			1273
Leu Trp Glu His Leu Ser Asn Gln Glu Ala Val Asp Leu Val Gln Lys			
290	295	300	
cat cca cac aat ggg att gct aga aga tta gta aaa gca gct ttg caa			1321
His Pro His Asn Gly Ile Ala Arg Arg Leu Val Lys Ala Ala Leu Gln			
305	310	315	320
gag gca gca aag aaa agg gaa atg agg tac tcg gat ttg aag aaa att			1369
Glu Ala Ala Lys Lys Arg Glu Met Arg Tyr Ser Asp Leu Lys Lys Ile			
325	330	335	
gac cgt ggg gtt cgc cgt cat ttc cat gat gac atc act gtt gtg gtg			1417
Asp Arg Gly Val Arg Arg His Phe His Asp Asp Ile Thr Val Val Val			
340	345	350	
gtg ttt ctt gac tca cac ctt gtg agc cgg gct agc tca gtc cgg ggc			1465
Val Phe Leu Asp Ser His Leu Val Ser Arg Ala Ser Ser Val Arg Gly			
355	360	365	
cca aac atc tcc gtg aaa ggt ggc ggc atc agt ctg cct ccc aat gct			1513
Pro Asn Ile Ser Val Lys Gly Gly Ile Ser Leu Pro Pro Asn Ala			
370	375	380	
ctt gca cct tgt gcc aca acg gag cca gtc cca aat tgatactgct			1562
Leu Ala Pro Cys Ala Thr Pro Thr Glu Pro Val Pro Asn			
385	390	395	
gtctttcta atgttatttc ccgttagtcc tgttgtacta ttgttatgtg aatacaggta			1622

gcttcttaac ggataaacgc ggcccttcaa ttctttaatc catactgtaa cttttaaccg 1682  
gagactatta cttggcatacg tttcaatgcc caagggatac atagactggg acaagccatc 1742  
ttggcggta caatcatcat agttaagttt tctgggcata tctttcaaaa aaaaaaaaaa 1802  
aaaaa 1806

<210> 34  
<211> 397  
<212> PRT  
<213> Avicennia marina

<400> 34  
Met Leu Ser Gly Leu Met Asn Phe Leu Trp Ala Cys Phe Arg Pro Arg  
1 5 10 15  
Ala Asp Arg Ser Val His Thr Gly Ser Asp Ala Gly Gly Arg Gln Asp  
20 25 30  
Gly Leu Leu Trp Tyr Lys Asp Leu Gly Gln His Ile Asn Gly Glu Phe  
35 40 45  
Ser Met Ala Val Val Gln Ala Asn Asn Leu Leu Glu Asp Gln Ser Gln  
50 55 60  
Leu Glu Ser Gly Cys Leu Ser Leu Ser Asp Ser Gly Gln Tyr Gly Thr  
65 70 75 80  
Phe Val Gly Ile Tyr Asp Gly His Gly Gly Pro Glu Thr Ser Arg Phe  
85 90 95  
Ile Asn Asp His Leu Phe Gln His Ile Lys Arg Phe Thr Ala Glu His  
100 105 110  
Gln Ser Met Ser Ala Glu Val Ile His Lys Ala Ile Gln Ala Thr Glu  
115 120 125  
Glu Gly Phe Phe Ser Val Val Ser Arg Gln Trp Ser Met Gln Pro Gln  
130 135 140  
Ile Ala Ala Val Gly Ser Cys Cys Leu Val Gly Val Ile Cys Ser Gly  
145 150 155 160  
Thr Leu Tyr Val Ser Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Thr  
165 170 175  
Leu Ser Lys Ala Thr Gly Glu Val Gln Ala Thr Gln Leu Ser Thr Glu  
180 185 190  
His Asn Ala Ser Phe Glu Ser Val Arg Arg Glu Leu Gln Ser Leu His  
195 200 205  
Pro Asp Asp Ser Gln Ile Val Val Leu Lys His Asn Val Trp Arg Val  
210 215 220

Lys Gly Leu Ile Gln Ile Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys  
 225 230 235 240  
 Lys Ala Glu Phe Asn Arg Glu Pro Leu Tyr Gln Lys Phe Arg Leu Arg  
 245 250 255  
 Glu Ala Phe Lys Arg Pro Ile Leu Ser Ser Glu Pro Glu Thr Thr Val  
 260 265 270  
 His Gln Leu Leu Pro His Asp Gln Phe Ile Ile Phe Ala Ser Asp Gly  
 275 280 285  
 Leu Trp Glu His Leu Ser Asn Gln Glu Ala Val Asp Leu Val Gln Lys  
 290 295 300  
 His Pro His Asn Gly Ile Ala Arg Arg Leu Val Lys Ala Ala Leu Gln  
 305 310 315 320  
 Glu Ala Ala Lys Lys Arg Glu Met Arg Tyr Ser Asp Leu Lys Lys Ile  
 325 330 335  
 Asp Arg Gly Val Arg Arg His Phe His Asp Asp Ile Thr Val Val Val  
 340 345 350  
 Val Phe Leu Asp Ser His Leu Val Ser Arg Ala Ser Ser Val Arg Gly  
 355 360 365  
 Pro Asn Ile Ser Val Lys Gly Gly Ile Ser Leu Pro Pro Asn Ala  
 370 375 380  
 Leu Ala Pro Cys Ala Thr Pro Thr Glu Pro Val Pro Asn  
 385 390 395

<210> 35  
 <211> 743  
 <212> DNA  
 <213> *Mesembryanthemum crystallinum*

<220>  
 <221> CDS  
 <222> (1)..(420)

<400> 35  
 cct gag cta gca cct aaa gat ggg gat ttc cgt ttc aat atc tct gag 48  
 Pro Glu Leu Ala Pro Lys Asp Gly Asp Phe Arg Phe Asn Ile Ser Glu  
 1 5 10 15  
 ctt gaa gct atg cta cca gct gga act gta gat cat gct gtt gaa agg 96  
 Leu Glu Ala Met Leu Pro Ala Gly Thr Val Asp His Ala Val Glu Arg  
 20 25 30  
 att tat caa gag atg ccg cgg tgg gaa gag act gtt tta ggt tcc agg 144  
 Ile Tyr Gln Glu Met Pro Arg Trp Glu Glu Thr Val Leu Gly Ser Arg  
 35 40 45

agc aga tat gag cat gtc att cag gca ctt gca gat aaa tac cct tca	192
Ser Arg Tyr Glu His Val Ile Gln Ala Leu Ala Asp Lys Tyr Pro Ser	
50 55 60	
gaa aat ttg ttg cta gtt acg cat ggt gaa ggt gtt ggg act tca gtt	240
Glu Asn Leu Leu Val Thr His Gly Glu Gly Val Gly Thr Ser Val	
65 70 75 80	
gca acg ttt ttg aaa ggc gct gtt gtt tat gaa gta aag tat tgt gct	288
Ala Thr Phe Leu Lys Gly Ala Val Val Tyr Glu Val Lys Tyr Cys Ala	
85 90 95	
tat tca caa gca aca aga cgc atc agc tat gga gaa ggc gag tca ttt	336
Tyr Ser Gln Ala Thr Arg Arg Ile Ser Tyr Gly Glu Ser Phe	
100 105 110	
act gct ggt acc ttt cag ttg gtc act gcc tca gac caa acc ggt att	384
Thr Ala Gly Thr Phe Gln Leu Val Thr Ala Ser Asp Gln Thr Gly Ile	
115 120 125	
ggc tac tac aca tct agc agc ttg tct gat ggt gta tgacttatcg	430
Gly Tyr Tyr Thr Ser Ser Ser Leu Ser Asp Gly Val	
130 135 140	
gaactcccgaa gtttctgcat tctgaaaggt gcttttgat ttccgaataa ttcttcaaata 490	
ccacatgtca gaagatccat tcttaggtc agatgtctat ctactgctcc cagccttgag 550	
ctgctcatgg gtattggtgc ctttctat ttaggttagag tctttgagta agccttgcca 610	
catcaaggcc tcagattatt gaatgtacaa cagaataggt ttagcttca ttggcttagta 670	
cagtgacctc tttcatgggt ctgaaacatc aatataaagg tttgaatggc aaaaaaaaaa 730	
aaaaaaaaaaa aaa	743

<210> 36  
 <211> 140  
 <212> PRT  
 <213> *Mesembryanthemum crystallinum*

<400> 36  
 Pro Glu Leu Ala Pro Lys Asp Gly Asp Phe Arg Phe Asn Ile Ser Glu  
 1 5 10 15

Leu Glu Ala Met Leu Pro Ala Gly Thr Val Asp His Ala Val Glu Arg  
 20 25 30

Ile Tyr Gln Glu Met Pro Arg Trp Glu Glu Thr Val Leu Gly Ser Arg  
 35 40 45

Ser Arg Tyr Glu His Val Ile Gln Ala Leu Ala Asp Lys Tyr Pro Ser  
 50 55 60

Glu Asn Leu Leu Val Thr His Gly Glu Gly Val Gly Thr Ser Val  
 65 70 75 80

Ala Thr Phe Leu Lys Gly Ala Val Val Tyr Glu Val Lys Tyr Cys Ala  
85 90 95

Tyr Ser Gln Ala Thr Arg Arg Ile Ser Tyr Gly Glu Gly Glu Ser Phe  
100 105 110

Thr Ala Gly Thr Phe Gln Leu Val Thr Ala Ser Asp Gln Thr Gly Ile  
115 120 125

Gly Tyr Tyr Thr Ser Ser Ser Leu Ser Asp Gly Val  
130 135 140

<210> 37

<211> 348

<212> DNA

<213> Sueada japonica

<220>

<221> CDS

<222> (1)...(246)

<400> 37

atc att gct ccc cta gct att ggt ttg atc gtt ggt gcc aac atc tta 48  
Ile Ile Ala Pro Leu Ala Ile Gly Leu Ile Val Gly Ala Asn Ile Leu  
1 5 10 15

gcc gga ggt gca ttt gat ggt gcc tca atg aac cct gcc gtc tct ttt 96  
Ala Gly Gly Ala Phe Asp Gly Ala Ser Met Asn Pro Ala Val Ser Phe  
20 25 30

ggc ccc gcc gtg gtt agc tgg agc tgg gcc aac cac tgg gtc tac tgg 144  
Gly Pro Ala Val Val Ser Trp Ser Trp Ala Asn His Trp Val Tyr Trp  
35 40 45

gca ggc cca ctc att ggt ggt gga ctt gct ggt ctc gtt tat gag ttt 192  
Ala Gly Pro Leu Ile Gly Gly Leu Ala Gly Leu Val Tyr Glu Phe  
50 55 60

atc ttt att ggt cac caa gag cca gct tcc gct gac tac cag aga ctc 240  
Ile Phe Ile Gly His Gln Glu Pro Ala Ser Ala Asp Tyr Gln Arg Leu  
65 70 75 80

tct gct taagaatttt aattctttgc cctaggaaaa aatgtttcat gcatgtattt 296  
Ser Ala

tggattttg ttgggtctaa aattttatga agggaaaaaa aaaaaaaaaa aa 348

<210> 38

<211> 82

<212> PRT

<213> Sueada japonica

<400> 38

Ile Ile Ala Pro Leu Ala Ile Gly Leu Ile Val Gly Ala Asn Ile Leu  
1 5 10 15

Ala Gly Gly Ala Phe Asp Gly Ala Ser Met Asn Pro Ala Val Ser Phe  
20 25 30

Gly Pro Ala Val Val Ser Trp Ser Trp Ala Asn His Trp Val Tyr Trp  
35 40 45

Ala Gly Pro Leu Ile Gly Gly Leu Ala Gly Leu Val Tyr Glu Phe  
50 55 60

Ile Phe Ile Gly His Gln Glu Pro Ala Ser Ala Asp Tyr Gln Arg Leu  
65 70 75 80

Ser Ala

<210> 39

<211> 1602

<212> DNA

<213> Sueada japonica

<220>

<221> CDS

<222> (1)..(1419)

<400> 39

cac acc gtt gat tta acc att gaa gct atg atg ctc gat tct caa gct 48  
His Thr Val Asp Leu Thr Ile Glu Ala Met Met Leu Asp Ser Gln Ala  
1 5 10 15

tct gat ctt gac aaa gaa cgt cct gag att ctt tca atg ctt ccg 96  
Ser Asp Leu Asp Lys Glu Glu Arg Pro Glu Ile Leu Ser Met Leu Pro  
20 25 30

cct ctt gaa gga aaa tgc ctc ttg gaa ctt ggg gct ggt att ggt cgt 144  
Pro Leu Glu Gly Lys Cys Leu Leu Glu Leu Gly Ala Gly Ile Gly Arg  
35 40 45

ttt act ggt gaa ttg gct gag aaa gct ggc cag gtt att gct ctg gat 192  
Phe Thr Gly Glu Leu Ala Glu Lys Ala Gly Gln Val Ile Ala Leu Asp  
50 55 60

ttc att gag agt gct atc aag aag aat gaa gta atc aat ggg cac tac 240  
Phe Ile Glu Ser Ala Ile Lys Lys Asn Glu Val Ile Asn Gly His Tyr  
65 70 75 80

aaa aat gtc aag ttt atg tgt gct gat gtg act tct ccc act ctc agt 288  
Lys Asn Val Lys Phe Met Cys Ala Asp Val Thr Ser Pro Thr Leu Ser  
85 90 95

ttc cca cca cat tca ttg gat gtg ata ttc tcc aat tgg tta ctc atg 336  
Phe Pro Pro His Ser Leu Asp Val Ile Phe Ser Asn Trp Leu Leu Met  
100 105 110

tat ctt tct gat gaa gag gtg gaa aat ttg gtt gaa aga atg ttg aaa		384	
Tyr Leu Ser Asp Glu Glu Val Glu Asn Leu Val Glu Arg Met Leu Lys			
115	120	125	
tgg ttg aag cca ggg ggt tac att ttc ttc aga gaa tct tgt ttc cat		432	
Trp Leu Lys Pro Gly Gly Tyr Ile Phe Phe Arg Glu Ser Cys Phe His			
130	135	140	
caa tct ggg gat cac aaa cgc aaa agc aat ccc acc cac tac cgt gaa		480	
Gln Ser Gly Asp His Lys Arg Lys Ser Asn Pro Thr His Tyr Arg Glu			
145	150	155	160
cct agg ttc tac act aag gcc ttc aaa gag tgt cat ttg caa gat gga		528	
Pro Arg Phe Tyr Thr Lys Ala Phe Lys Glu Cys His Leu Gln Asp Gly			
165	170	175	
tct gga aac tct tat gag ctc tcc cta ctt agc tgc aaa tgt att gga		576	
Ser Gly Asn Ser Tyr Glu Leu Ser Leu Leu Ser Cys Lys Cys Ile Gly			
180	185	190	
gct tat gtc aga aac aag aaa aac cag aac cag att agt tgg ttg tgg		624	
Ala Tyr Val Arg Asn Lys Lys Asn Gln Asn Gln Ile Ser Trp Leu Trp			
195	200	205	
caa aaa gtt gat tct aag gat gat aag ggg ttc cag cga ttt ctg gat		672	
Gln Lys Val Asp Ser Lys Asp Asp Lys Gly Phe Gln Arg Phe Leu Asp			
210	215	220	
act agc cag tac aag tgt aat agc att ctg cga tat gag cgt gta ttt		720	
Thr Ser Gln Tyr Lys Cys Asn Ser Ile Leu Arg Tyr Glu Arg Val Phe			
225	230	235	240
ggc cct ggt tat gtt agc act gga gga tat gaa acc acc aaa gag ttt		768	
Gly Pro Gly Tyr Val Ser Thr Gly Gly Tyr Glu Thr Thr Lys Glu Phe			
245	250	255	
gtg tca atg ctg gac ttg aag cct ggc cag aag gtc ctg gat gtt ggt		816	
Val Ser Met Leu Asp Leu Lys Pro Gly Gln Lys Val Leu Asp Val Gly			
260	265	270	
tgt gga att ggt gga ggt gac ttt tac atg gcg gag acc ttt gat gtt		864	
Cys Gly Ile Gly Gly Asp Phe Tyr Met Ala Glu Thr Phe Asp Val			
275	280	285	
gag gtt ggt gga ttt gat ctc tcc gtt aat atg att tcc ttt gcc ctt		912	
Glu Val Val Gly Phe Asp Leu Ser Val Asn Met Ile Ser Phe Ala Leu			
290	295	300	
gag cgt tct att ggg ctt aaa tgt gct gtt gag ttt gag gta gca gat		960	
Glu Arg Ser Ile Gly Leu Lys Cys Ala Val Glu Phe Glu Val Ala Asp			
305	310	315	320
tgc acc aag ata aac tac cct gat aac tct ttt gat gtc atc tat agc		1008	
Cys Thr Lys Ile Asn Tyr Pro Asp Asn Ser Phe Asp Val Ile Tyr Ser			
325	330	335	

cgt gac acc att ctg cat att cag gac aag cct gcg ttg ttt aga tcc 1056  
 Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro Ala Leu Phe Arg Ser  
 340 345 350  
  
 ttc tac aaa tgg ttg aag cca gga ggt aaa gtt cta atc agt gat tac 1104  
 Phe Tyr Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Ser Asp Tyr  
 355 360 365  
  
 tgc aag aaa gct ggt cca ccc tca cct gaa ttc gcc gct tac att aag 1152  
 Cys Lys Lys Ala Gly Pro Pro Ser Pro Glu Phe Ala Ala Tyr Ile Lys  
 370 375 380  
  
 cag agg gga tat gat ctc cat gat gta aag gaa tat ggg cag atg ctt 1200  
 Gln Arg Gly Tyr Asp Leu His Asp Val Lys Glu Tyr Gly Gln Met Leu  
 385 390 395 400  
  
 aaa gat gct gga ttt gtt gat gtt ctt gcc gag gat aga act gag cag 1248  
 Lys Asp Ala Gly Phe Val Asp Val Leu Ala Glu Asp Arg Thr Glu Gln  
 405 410 415  
  
 ttc att cga gtt cta cgg aag gaa cta gag act gtt gag aag gaa aag 1296  
 Phe Ile Arg Val Leu Arg Lys Glu Leu Glu Thr Val Glu Lys Glu Lys  
 420 425 430  
  
 gat gtg ttc att agt gat ttc tct gag gag gat tac aat gac att gtt 1344  
 Asp Val Phe Ile Ser Asp Phe Ser Glu Glu Asp Tyr Asn Asp Ile Val  
 435 440 445  
  
 gga ggt tgg aat gat aag ttg cgg agg act gcc aag ggt gag caa cga 1392  
 Gly Gly Trp Asn Asp Lys Leu Arg Arg Thr Ala Lys Gly Glu Gln Arg  
 450 455 460  
  
 tgg ggt ctg ttc gtt gcc aag aag aag tgaagaatca gttgccgcac 1439  
 Trp Gly Leu Phe Val Ala Lys Lys Lys  
 465 470  
  
 tggcactgtc gatttccttag tattaatctt caatgttttc atgtaatgta cttctacatg 1499  
  
 taaaattgcc aataagttgc atttcgcaga ctgtaagatg attaatcata ttttatctt 1559  
  
 taattaatca tggattttatg caaaaaaaaaaaa aaaaaaaaaaaa aaa 1602  
  
 <210> 40  
 <211> 473  
 <212> PRT  
 <213> Sueada japonica  
  
 <400> 40  
 His Thr Val Asp Leu Thr Ile Glu Ala Met Met Leu Asp Ser Gln Ala  
 1 5 10 15  
  
 Ser Asp Leu Asp Lys Glu Glu Arg Pro Glu Ile Leu Ser Met Leu Pro  
 20 25 30  
  
 Pro Leu Glu Gly Lys Cys Leu Leu Glu Leu Gly Ala Gly Ile Gly Arg  
 35 40 45

Phe Thr Gly Glu Leu Ala Glu Lys Ala Gly Gln Val Ile Ala Leu Asp  
50 55 60

Phe Ile Glu Ser Ala Ile Lys Lys Asn Glu Val Ile Asn Gly His Tyr  
65 70 75 80

Lys Asn Val Lys Phe Met Cys Ala Asp Val Thr Ser Pro Thr Leu Ser  
85 90 95

Phe Pro Pro His Ser Leu Asp Val Ile Phe Ser Asn Trp Leu Leu Met  
100 105 110

Tyr Leu Ser Asp Glu Glu Val Glu Asn Leu Val Glu Arg Met Leu Lys  
115 120 125

Trp Leu Lys Pro Gly Gly Tyr Ile Phe Phe Arg Glu Ser Cys Phe His  
130 135 140

Gln Ser Gly Asp His Lys Arg Lys Ser Asn Pro Thr His Tyr Arg Glu  
145 150 155 160

Pro Arg Phe Tyr Thr Lys Ala Phe Lys Glu Cys His Leu Gln Asp Gly  
165 170 175

Ser Gly Asn Ser Tyr Glu Leu Ser Leu Leu Ser Cys Lys Cys Ile Gly  
180 185 190

Ala Tyr Val Arg Asn Lys Lys Asn Gln Asn Gln Ile Ser Trp Leu Trp  
195 200 205

Gln Lys Val Asp Ser Lys Asp Asp Lys Gly Phe Gln Arg Phe Leu Asp  
210 215 220

Thr Ser Gln Tyr Lys Cys Asn Ser Ile Leu Arg Tyr Glu Arg Val Phe  
225 230 235 240

Gly Pro Gly Tyr Val Ser Thr Gly Gly Tyr Glu Thr Thr Lys Glu Phe  
245 250 255

Val Ser Met Leu Asp Leu Lys Pro Gly Gln Lys Val Leu Asp Val Gly  
260 265 270

Cys Gly Ile Gly Gly Asp Phe Tyr Met Ala Glu Thr Phe Asp Val  
275 280 285

Glu Val Val Gly Phe Asp Leu Ser Val Asn Met Ile Ser Phe Ala Leu  
290 295 300

Glu Arg Ser Ile Gly Leu Lys Cys Ala Val Glu Phe Glu Val Ala Asp  
305 310 315 320

Cys Thr Lys Ile Asn Tyr Pro Asp Asn Ser Phe Asp Val Ile Tyr Ser  
325 330 335

Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro Ala Leu Phe Arg Ser  
340 345 350

Phe Tyr Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Ser Asp Tyr  
 355 360 365  
 Cys Lys Lys Ala Gly Pro Pro Ser Pro Glu Phe Ala Ala Tyr Ile Lys  
 370 375 380  
 Gln Arg Gly Tyr Asp Leu His Asp Val Lys Glu Tyr Gly Gln Met Leu  
 385 390 395 400  
 Lys Asp Ala Gly Phe Val Asp Val Leu Ala Glu Asp Arg Thr Glu Gln  
 405 410 415  
 Phe Ile Arg Val Leu Arg Lys Glu Leu Glu Thr Val Glu Lys Glu Lys  
 420 425 430  
 Asp Val Phe Ile Ser Asp Phe Ser Glu Glu Asp Tyr Asn Asp Ile Val  
 435 440 445  
 Gly Gly Trp Asn Asp Lys Leu Arg Arg Thr Ala Lys Gly Glu Gln Arg  
 450 455 460  
 Trp Gly Leu Phe Val Ala Lys Lys Lys  
 465 470

<210> 41  
 <211> 1251  
 <212> DNA  
 <213> Salsola komarovii

<220>  
 <221> CDS  
 <222> (1)...(933)

<400> 41  
 cag cca ttt ggc aca att aat gga tca ctt cgt gtt act gta caa ggt 48  
 Gln Pro Phe Gly Thr Ile Asn Gly Ser Leu Arg Val Thr Val Gln Gly  
 1 5 10 15

gag gtc att gaa caa tct ttt gga gag gag cac ttg tgt ttt aga aca 96  
 Glu Val Ile Glu Gln Ser Phe Gly Glu Glu His Leu Cys Phe Arg Thr  
 20 25 30

tta cag cgg tac aca gct gcc aca ctt gag cat gga atg cat cca cca 144  
 Leu Gln Arg Tyr Thr Ala Ala Thr Leu Glu His Gly Met His Pro Pro  
 35 40 45

atc tct cct aaa cca gaa tgg cgt gca ctt ttg gac gag atg gct gtt 192  
 Ile Ser Pro Lys Pro Glu Trp Arg Ala Leu Leu Asp Glu Met Ala Val  
 50 55 60

gtt gcc acc aag gaa tac cgc tct gtt gtt ttt cat gag cct cgc ttt 240  
 Val Ala Thr Lys Glu Tyr Arg Ser Val Val Phe His Glu Pro Arg Phe  
 65 70 75 80

gtc gag tac ttc cgc agt gct aca cca gag aca gag tat ggg cgt atg	288
Val Glu Tyr Phe Arg Ser Ala Thr Pro Glu Thr Glu Tyr Gly Arg Met	
85 90 95	
aat att gga agc cgt cct gca aag aga aag cca gga gga gga att gaa	336
Asn Ile Gly Ser Arg Pro Ala Lys Arg Lys Pro Gly Gly Ile Glu	
100 105 110	
act ctg cgt gca att cct tgg ata ttt tcg tgg aca caa acc agg ttt	384
Thr Leu Arg Ala Ile Pro Trp Ile Phe Ser Trp Thr Gln Thr Arg Phe	
115 120 125	
cat tta cct gtg tgg ctt ggg gtt gga gca gct ttt aag cat gcc ctt	432
His Leu Pro Val Trp Leu Gly Val Gly Ala Ala Phe Lys His Ala Leu	
130 135 140	
gac aag gac att aag aat ctt tcg ata ctc aag gcc atg tat aat gag	480
Asp Lys Asp Ile Lys Asn Leu Ser Ile Leu Lys Ala Met Tyr Asn Glu	
145 150 155 160	
tgg ccg ttc ttc aga gtg act att gat ctc tta gaa atg gtt ttc act	528
Trp Pro Phe Phe Arg Val Thr Ile Asp Leu Leu Glu Met Val Phe Thr	
165 170 175	
aaa gga gac cct gga att gct gct tta tat gac aag ctt ctg gtg gca	576
Lys Gly Asp Pro Gly Ile Ala Ala Leu Tyr Asp Lys Leu Leu Val Ala	
180 185 190	
gag gat ttg aag ccc ttt ggg gaa aag ttg agg aaa agt ttc gaa gat	624
Glu Asp Leu Lys Pro Phe Gly Glu Lys Leu Arg Lys Ser Phe Glu Asp	
195 200 205	
acc aaa ctc ctt ctc ctt aag gtt gct ggg cac aag gag tta ctg gaa	672
Thr Lys Leu Leu Leu Lys Val Ala Gly His Lys Glu Leu Leu Glu	
210 215 220	
gga gat cct tac ttg aaa cag aga ctc cga ctt cgt gat cct tac att	720
Gly Asp Pro Tyr Leu Lys Gln Arg Leu Arg Asp Pro Tyr Ile	
225 230 235 240	
aca acc ctt aat gtt ttc caa gca tat act ctg aag cgg atc cgt gat	768
Thr Thr Leu Asn Val Phe Gln Ala Tyr Thr Leu Lys Arg Ile Arg Asp	
245 250 255	
ccc aat ttc cat gta gct gaa ggg cca cac tta tcc aag gaa gta ttg	816
Pro Asn Phe His Val Ala Glu Gly Pro His Leu Ser Lys Glu Val Leu	
260 265 270	
gaa tca aac aat gct gag ctt gtg aag ctc aat cct act agt gag tat	864
Glu Ser Asn Asn Ala Glu Leu Val Lys Leu Asn Pro Thr Ser Glu Tyr	
275 280 285	
cct cct ggc ctt gag gac acc ctt atc ttg acc atg aag ggt att gct	912
Pro Pro Gly Leu Glu Asp Thr Leu Ile Leu Thr Met Lys Gly Ile Ala	
290 295 300	
gct ggc atg cag aac acc ggt taactgacac gtgttgacac tctattgcaa	963

Ala Gly Met Gln Asn Thr Gly  
305 310

ctattcctca actccttctg gtttggggat ccgggctcg agatagccat cgttggtgat 1023  
gtgctgtatg agcaccta atgttattcaaa gtctgtat tt caagtctatt gtatttgat 1083  
tttggcttc tttatgtttt ttatgttctt acttatggtt gggttgtgtc acttggact 1143  
aataccgac tgtgtataaa atgggtgtt tactgatgaa cagttgttt tcttctacgt 1203  
gagttatatt gatgagttt tcttttatta aaaaaaaaaa aaaaaaaaaa 1251

<210> 42  
<211> 311  
<212> PRT  
<213> Salsola komarovii

<400> 42  
Gln Pro Phe Gly Thr Ile Asn Gly Ser Leu Arg Val Thr Val Gln Gly  
1 5 10 15

Glu Val Ile Glu Gln Ser Phe Gly Glu Glu His Leu Cys Phe Arg Thr  
20 25 30

Leu Gln Arg Tyr Thr Ala Ala Thr Leu Glu His Gly Met His Pro Pro  
35 40 45

Ile Ser Pro Lys Pro Glu Trp Arg Ala Leu Leu Asp Glu Met Ala Val  
50 55 60

Val Ala Thr Lys Glu Tyr Arg Ser Val Val Phe His Glu Pro Arg Phe  
65 70 75 80

Val Glu Tyr Phe Arg Ser Ala Thr Pro Glu Thr Glu Tyr Gly Arg Met  
85 90 95

Asn Ile Gly Ser Arg Pro Ala Lys Arg Lys Pro Gly Gly Ile Glu  
100 105 110

Thr Leu Arg Ala Ile Pro Trp Ile Phe Ser Trp Thr Gln Thr Arg Phe  
115 120 125

His Leu Pro Val Trp Leu Gly Val Gly Ala Ala Phe Lys His Ala Leu  
130 135 140

Asp Lys Asp Ile Lys Asn Leu Ser Ile Leu Lys Ala Met Tyr Asn Glu  
145 150 155 160

Trp Pro Phe Phe Arg Val Thr Ile Asp Leu Leu Glu Met Val Phe Thr  
165 170 175

Lys Gly Asp Pro Gly Ile Ala Ala Leu Tyr Asp Lys Leu Leu Val Ala  
180 185 190

Glu Asp Leu Lys Pro Phe Gly Glu Lys Leu Arg Lys Ser Phe Glu Asp

195

200

205

Thr Lys Leu Leu Leu Leu Lys Val Ala Gly His Lys Glu Leu Leu Glu  
 210 215 220

Gly Asp Pro Tyr Leu Lys Gln Arg Leu Arg Leu Arg Asp Pro Tyr Ile  
 225 230 235 240

Thr Thr Leu Asn Val Phe Gln Ala Tyr Thr Leu Lys Arg Ile Arg Asp  
 245 250 255

Pro Asn Phe His Val Ala Glu Gly Pro His Leu Ser Lys Glu Val Leu  
 260 265 270

Glu Ser Asn Asn Ala Glu Leu Val Lys Leu Asn Pro Thr Ser Glu Tyr  
 275 280 285

Pro Pro Gly Leu Glu Asp Thr Leu Ile Leu Thr Met Lys Gly Ile Ala  
 290 295 300

Ala Gly Met Gln Asn Thr Gly  
 305 310

<210> 43  
 <211> 637  
 <212> DNA  
 <213> Avicennia marina

<220>  
 <221> CDS  
 <222> (1)...(339)

<400> 43  
 caa tac ttg gta aat gaa gtg aag aaa act gtt cag ggg cgt gct caa 48  
 Gln Tyr Leu Val Asn Glu Val Lys Lys Thr Val Gln Gly Arg Ala Gln  
 1 5 10 15

ctt ggt gtg gaa gca ttt gct gat gcg ctt ctt gtg gtt cca aag acg 96  
 Leu Gly Val Glu Ala Phe Ala Asp Ala Leu Leu Val Val Pro Lys Thr  
 20 25 30

ctt gcc gag aac tct ggc ctt gat acc cag gat ttg att att gaa ctt 144  
 Leu Ala Glu Asn Ser Gly Leu Asp Thr Gln Asp Leu Ile Ile Glu Leu  
 35 40 45

acg gga gaa tat gaa aaa ggg aat gtg gta gga ctt aat cta cac aca 192  
 Thr Gly Glu Tyr Glu Lys Gly Asn Val Val Gly Leu Asn Leu His Thr  
 50 55 60

gga gaa cct ata gat cct caa atg gag ggt atc ttt gac aat tat tcc 240  
 Gly Glu Pro Ile Asp Pro Gln Met Glu Gly Ile Phe Asp Asn Tyr Ser  
 65 70 75 80

gtg aag cgt cag atc ata aac tca ggc ccc gtt att gca tct cag ctg 288  
 Val Lys Arg Gln Ile Ile Asn Ser Gly Pro Val Ile Ala Ser Gln Leu

85

90

95

cta ctt gtc gac gag gtt att cgt gct ggt cgt aac atg cgt aaa ccg 336  
 Leu Leu Val Asp Glu Val Ile Arg Ala Gly Arg Asn Met Arg Lys Pro  
 100 105 110

aat tagcttcac cctagttttt gtgatgttgg tgaagatggg aattttat 389  
 Asn

aggttagggc atggttcctt ttgttagcc taagcaactat gtattcattt ccacttgaga 449  
 tttgaattttt gatcatcagg cggttgaact tttcgccgt tacaaattgc accagaaatt 509  
 attcgaccat gggtatgcat ctacttgtgt tgtacctgac ttggctaagt tatttgaaga 569  
 tacactctgt gctcagcaaa gaattggaaa aaaaggaatt gatttcatca aaaaaaaaaa 629  
 aaaaaaaaaa 637

<210> 44  
 <211> 113  
 <212> PRT  
 <213> Avicennia marina

<400> 44  
 Gln Tyr Leu Val Asn Glu Val Lys Lys Thr Val Gln Gly Arg Ala Gln  
 1 5 10 15

Leu Gly Val Glu Ala Phe Ala Asp Ala Leu Leu Val Val Pro Lys Thr  
 20 25 30

Leu Ala Glu Asn Ser Gly Leu Asp Thr Gln Asp Leu Ile Ile Glu Leu  
 35 40 45

Thr Gly Glu Tyr Glu Lys Gly Asn Val Val Gly Leu Asn Leu His Thr  
 50 55 60

Gly Glu Pro Ile Asp Pro Gln Met Glu Gly Ile Phe Asp Asn Tyr Ser  
 65 70 75 80

Val Lys Arg Gln Ile Ile Asn Ser Gly Pro Val Ile Ala Ser Gln Leu  
 85 90 95

Leu Leu Val Asp Glu Val Ile Arg Ala Gly Arg Asn Met Arg Lys Pro  
 100 105 110

Asn

<210> 45  
 <211> 741  
 <212> DNA  
 <213> Avicennia marina

<220>  
<221> CDS  
<222> (3)...(293)

<400> 45  
aa gag atc aat tgt ctt gaa tgg gag aac ttt gct ttc cat ccc agc 47  
Glu Ile Asn Cys Leu Glu Trp Glu Asn Phe Ala Phe His Pro Ser  
1 5 10 15  
  
cca ctc att gtt ctt gtt ttt gaa aga tac aac agg gca agt gat aac 95  
Pro Leu Ile Val Leu Val Phe Glu Arg Tyr Asn Arg Ala Ser Asp Asn  
20 25 30  
  
tgg aaa gct ttg aag gag ttg gaa aag gcg gca gaa gtt tac tgg aag 143  
Trp Lys Ala Leu Lys Glu Leu Glu Lys Ala Ala Glu Val Tyr Trp Lys  
35 40 45  
  
gca aaa gat cga ctg cct cct cggt acg gtc aag ata gat ata aac atc 191  
Ala Lys Asp Arg Leu Pro Pro Arg Thr Val Lys Ile Asp Ile Asn Ile  
50 55 60  
  
gaa agg gat tta gca tat gca ctc aag gtt aaa gaa tgc ccg cag ata 239  
Glu Arg Asp Leu Ala Tyr Ala Leu Lys Val Lys Glu Cys Pro Gln Ile  
65 70 75  
  
ctg ttc tta cgc gga aac agg ata tta tac aga gag aaa ggt agc cca 287  
Leu Phe Leu Arg Gly Asn Arg Ile Leu Tyr Arg Glu Lys Gly Ser Pro  
80 85 90 95  
  
ttt ctc tgatattgca tgtacatcag atctttcaat ctgcaccaga accaatttag 343  
Phe Leu  
  
tttaccatca tttccagaaa ttagatcatc ggatgaattt gttcagatga tcgcgcattt 403  
ctattacaat gcaaaaaagc ctgcgtgcattt cgtatgtca gctttctt caccacatca 463  
ctgaaggtga ggttgtcaaa tggaaatccag catcagtcat tagggaggac tgaagctgta 523  
cgaggaaag tggtttaat tcagatttgg tctttgaagt gggcagtgg gattgaaacg 583  
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25

30

Lys Ala Leu Lys Glu Leu Glu Lys Ala Ala Glu Val Tyr Trp Lys Ala  
35 40 45

Lys Asp Arg Leu Pro Pro Arg Thr Val Lys Ile Asp Ile Asn Ile Glu  
50 55 60

Arg Asp Leu Ala Tyr Ala Leu Lys Val Lys Glu Cys Pro Gln Ile Leu  
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Phe Leu Arg Gly Asn Arg Ile Leu Tyr Arg Glu Lys Gly Ser Pro Phe  
, P

, R, Q□^, X, P

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90

95

Leu

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1 5 10 15

ctc ttc ttc tct ctc cta ata ttc ctt tca tct gct aat ctt tat cat 96  
 Leu Phe Phe Ser Leu Leu Ile Phe Leu Ser Ser Ala Asn Leu Tyr His  
 20 25 30

cag aat caa gga tct tgt agt gac ttt gaa tca gaa cca tca atg gct 144  
 Gln Asn Gln Gly Ser Cys Ser Asp Phe Glu Ser Glu Pro Ser Met Ala  
           35                 40                 45

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act ctt ggt gga ttg cgc gaa tcc cat ggt gct tct aat gat gct gag 192
Thr Leu Gly Gly Leu Arg Glu Ser His Gly Ala Ser Asn Asp Ala Glu
      50           55           60

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att gaa acc ctt gct cgc ttt gct gtt gat gaa cac aac aaa aaa gag	240
Ile Glu Thr Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu	
65 70 75 80	

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aat gca ttg ttg gag ttt gca agg gtt gta aag gca aag gaa cag gtg  288
Asn Ala Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val
85          90          95

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gtt gcg ggt aca ttg cat cac ttc act atc gaa gca att gaa gcg ggc  336
Val Ala Gly Thr Leu His His Phe Thr Ile Glu Ala Ile Glu Ala Gly
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aag aag aag ctc tac gaa gcg aag gtg tgg gtg aag cca tgg atg aac 384
Lys Lys Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn
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ttt aag gag ctg cag gaa ttt aag cat gct gat gaa tcc cct tca atc 432
Phe Lys Glu Leu Gln Glu Phe Lys His Ala Asp Glu Ser Pro Ser Ile
130           135           140

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act cct tcc gac ctc ggc gct aat aga gaa ggg cat tct gga gga tgg 480
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145           150           155           160

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aaa gat gtg cct gtc cat gac cct gaa gtg caa aat gca gca aat cat	528																																																		
Lys Asp Val Pro Val His Asp Pro Glu Val Gln Asn Ala Ala Asn His																																																			
165	170		175	gct ctt aag acc ttg caa caa aga tcc aac tcc tta ttt cct tat gaa	576	Ala Leu Lys Thr Leu Gln Gln Arg Ser Asn Ser Leu Phe Pro Tyr Glu		180	185		190	ctg cag gaa gtt gct cat gct agg gct gag gtt ctg gaa gac act gcg	624	Leu Gln Glu Val Ala His Ala Arg Ala Glu Val Leu Glu Asp Thr Ala		195	200		205	aag ttt aac ctg cac ctc aag gtg aag aga gga aac aag gat gag ttt	672	Lys Phe Asn Leu His Leu Lys Val Lys Arg Gly Asn Lys Asp Glu Phe		210	215		220	ttc aat gtg gag gtg cac aaa aac agc gaa gga aac tac aac ctt aat	720	Phe Asn Val Glu Val His Lys Asn Ser Glu Gly Asn Tyr Asn Leu Asn		225	230		235		240	cag atg ggg aac gtt gag ccc gag gtt gag aaa agt agt gtt	762	Gln Met Gly Asn Val Glu Pro Glu Val Glu Lys Ser Ser Val		245	250	tagactcggtt gaggggtgttg taagtactcg ttcgtaactt ttctgatggc caggcaagta	822	tggagtaagg actagactac tagtactagt aagtacagct gacttggttt gagtaaaaata	882	acctcgactt tgggtgcacc atcatatctt gtatgttat ggctttgtca atgtattgt	942	agtgaagatt gtttgcttga tctaaaaaaaaaaaaaaaaa a	983
	175																																																		
gct ctt aag acc ttg caa caa aga tcc aac tcc tta ttt cct tat gaa	576																																																		
Ala Leu Lys Thr Leu Gln Gln Arg Ser Asn Ser Leu Phe Pro Tyr Glu																																																			
180	185		190	ctg cag gaa gtt gct cat gct agg gct gag gtt ctg gaa gac act gcg	624	Leu Gln Glu Val Ala His Ala Arg Ala Glu Val Leu Glu Asp Thr Ala		195	200		205	aag ttt aac ctg cac ctc aag gtg aag aga gga aac aag gat gag ttt	672	Lys Phe Asn Leu His Leu Lys Val Lys Arg Gly Asn Lys Asp Glu Phe		210	215		220	ttc aat gtg gag gtg cac aaa aac agc gaa gga aac tac aac ctt aat	720	Phe Asn Val Glu Val His Lys Asn Ser Glu Gly Asn Tyr Asn Leu Asn		225	230		235		240	cag atg ggg aac gtt gag ccc gag gtt gag aaa agt agt gtt	762	Gln Met Gly Asn Val Glu Pro Glu Val Glu Lys Ser Ser Val		245	250	tagactcggtt gaggggtgttg taagtactcg ttcgtaactt ttctgatggc caggcaagta	822	tggagtaagg actagactac tagtactagt aagtacagct gacttggttt gagtaaaaata	882	acctcgactt tgggtgcacc atcatatctt gtatgttat ggctttgtca atgtattgt	942	agtgaagatt gtttgcttga tctaaaaaaaaaaaaaaaaa a	983								
	190																																																		
ctg cag gaa gtt gct cat gct agg gct gag gtt ctg gaa gac act gcg	624																																																		
Leu Gln Glu Val Ala His Ala Arg Ala Glu Val Leu Glu Asp Thr Ala																																																			
195	200		205	aag ttt aac ctg cac ctc aag gtg aag aga gga aac aag gat gag ttt	672	Lys Phe Asn Leu His Leu Lys Val Lys Arg Gly Asn Lys Asp Glu Phe		210	215		220	ttc aat gtg gag gtg cac aaa aac agc gaa gga aac tac aac ctt aat	720	Phe Asn Val Glu Val His Lys Asn Ser Glu Gly Asn Tyr Asn Leu Asn		225	230		235		240	cag atg ggg aac gtt gag ccc gag gtt gag aaa agt agt gtt	762	Gln Met Gly Asn Val Glu Pro Glu Val Glu Lys Ser Ser Val		245	250	tagactcggtt gaggggtgttg taagtactcg ttcgtaactt ttctgatggc caggcaagta	822	tggagtaagg actagactac tagtactagt aagtacagct gacttggttt gagtaaaaata	882	acctcgactt tgggtgcacc atcatatctt gtatgttat ggctttgtca atgtattgt	942	agtgaagatt gtttgcttga tctaaaaaaaaaaaaaaaaa a	983																
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aag ttt aac ctg cac ctc aag gtg aag aga gga aac aag gat gag ttt	672																																																		
Lys Phe Asn Leu His Leu Lys Val Lys Arg Gly Asn Lys Asp Glu Phe																																																			
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ttc aat gtg gag gtg cac aaa aac agc gaa gga aac tac aac ctt aat	720																																																		
Phe Asn Val Glu Val His Lys Asn Ser Glu Gly Asn Tyr Asn Leu Asn																																																			
225	230		235		240	cag atg ggg aac gtt gag ccc gag gtt gag aaa agt agt gtt	762	Gln Met Gly Asn Val Glu Pro Glu Val Glu Lys Ser Ser Val		245	250	tagactcggtt gaggggtgttg taagtactcg ttcgtaactt ttctgatggc caggcaagta	822	tggagtaagg actagactac tagtactagt aagtacagct gacttggttt gagtaaaaata	882	acctcgactt tgggtgcacc atcatatctt gtatgttat ggctttgtca atgtattgt	942	agtgaagatt gtttgcttga tctaaaaaaaaaaaaaaaaa a	983																																
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cag atg ggg aac gtt gag ccc gag gtt gag aaa agt agt gtt	762																																																		
Gln Met Gly Asn Val Glu Pro Glu Val Glu Lys Ser Ser Val																																																			
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	10		15	Leu Phe Phe Ser Leu Leu Ile Phe Leu Ser Ser Ala Asn Leu Tyr His		20	25		30	Gln Asn Gln Gly Ser Cys Ser Asp Phe Glu Ser Glu Pro Ser Met Ala		35	40		45	Thr Leu Gly Gly Leu Arg Glu Ser His Gly Ala Ser Asn Asp Ala Glu		50	55		60	Ile Glu Thr Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu		65	70		75		80	Asn Ala Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val		85	90		95		
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Leu Phe Phe Ser Leu Leu Ile Phe Leu Ser Ser Ala Asn Leu Tyr His																																					
20	25		30	Gln Asn Gln Gly Ser Cys Ser Asp Phe Glu Ser Glu Pro Ser Met Ala		35	40		45	Thr Leu Gly Gly Leu Arg Glu Ser His Gly Ala Ser Asn Asp Ala Glu		50	55		60	Ile Glu Thr Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu		65	70		75		80	Asn Ala Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val		85	90		95								
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Gln Asn Gln Gly Ser Cys Ser Asp Phe Glu Ser Glu Pro Ser Met Ala																																					
35	40		45	Thr Leu Gly Gly Leu Arg Glu Ser His Gly Ala Ser Asn Asp Ala Glu		50	55		60	Ile Glu Thr Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu		65	70		75		80	Asn Ala Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val		85	90		95														
	45																																				
Thr Leu Gly Gly Leu Arg Glu Ser His Gly Ala Ser Asn Asp Ala Glu																																					
50	55		60	Ile Glu Thr Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu		65	70		75		80	Asn Ala Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val		85	90		95																				
	60																																				
Ile Glu Thr Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu																																					
65	70		75		80	Asn Ala Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val		85	90		95																										
	75		80	Asn Ala Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val		85	90		95																												
	80																																				
Asn Ala Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val																																					
85	90		95																																		
	95																																				

Val Ala Gly Thr Leu His His Phe Thr Ile Glu Ala Ile Glu Ala Gly  
 100 105 110  
 Lys Lys Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn  
 115 120 125  
 Phe Lys Glu Leu Gln Glu Phe Lys His Ala Asp Glu Ser Pro Ser Ile  
 130 135 140  
 Thr Pro Ser Asp Leu Gly Ala Asn Arg Glu Gly His Ser Gly Gly Trp  
 145 150 155 160  
 Lys Asp Val Pro Val His Asp Pro Glu Val Gln Asn Ala Ala Asn His  
 165 170 175  
 Ala Leu Lys Thr Leu Gln Gln Arg Ser Asn Ser Leu Phe Pro Tyr Glu  
 180 185 190  
 Leu Gln Glu Val Ala His Ala Arg Ala Glu Val Leu Glu Asp Thr Ala  
 195 200 205  
 Lys Phe Asn Leu His Leu Lys Val Lys Arg Gly Asn Lys Asp Glu Phe  
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 Val Lys Gly Cys Leu Gly Ser Leu Asp Ser Ser Gly Lys Ser Thr Gly  
 20 25 30  
 agc ggc ggt aaa aaa cgt ggg ccc gct ccg tac aga atc tac aac ttg 143  
 Ser Gly Gly Lys Arg Gly Pro Ala Pro Tyr Arg Ile Tyr Asn Leu  
 35 40 45  
 ggg aac act caa ccg gtc act gta ccg aca ctt gtc ggt atc cta gag 191  
 Gly Asn Thr Gln Pro Val Thr Val Pro Thr Leu Val Gly Ile Leu Glu  
 50 55 60

aag cat ctc aaa gtt aag gcc aag aag aat gtg gtt gag atg ccc gga 239  
Lys His Leu Lys Val Lys Ala Lys Asn Val Val Glu Met Pro Gly  
65 70 75

aat ggt gac gtg ccc ttc aca cat gcg aat atc tct ttg gcc cga aaa 287  
Asn Gly Asp Val Pro Phe Thr His Ala Asn Ile Ser Leu Ala Arg Lys  
80 85 90 95

gat ttc ggg tat aaa ccc act acc gat ttg caa acc ggg ttg aaa aag 335  
Asp Phe Gly Tyr Lys Pro Thr Thr Asp Leu Gln Thr Gly Leu Lys Lys  
100 105 110

ttt gtt aga tgg tat ctc act tat tac ggc tac aac aac ggc aag cct 383  
Phe Val Arg Trp Tyr Leu Thr Tyr Tyr Gly Tyr Asn Asn Gly Lys Pro  
115 120 125

gta aat taatatataa atataagtaa tattttttt ctctttttt ataaaattaca 439  
Val Asn

gaattatTTT tttgggtgg tttatgaatt ttgttgata atatggggat tcttttttc 499  
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20 25 30

Gly Gly Lys Lys Arg Gly Pro Ala Pro Tyr Arg Ile Tyr Asn Leu Gly  
35 40 45

Asn Thr Gln Pro Val Thr Val Pro Thr Leu Val Gly Ile Leu Glu Lys  
50 55 60

His Leu Lys Val Lys Ala Lys Lys Asn Val Val Glu Met Pro Gly Asn  
65 70 75 80

Gly Asp Val Pro Phe Thr His Ala Asn Ile Ser Leu Ala Arg Lys Asp  
85 90 95

Phe Gly Tyr Lys Pro Thr Thr Asp Leu Gln Thr Gly Leu Lys Lys Phe  
100 105 110

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Asn

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<213> Sueada japonica

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1 5 10 15

gct aaa gga gtt gta gta gtt ctc act tct aga gat gga aaa aga ggc 97  
Ala Lys Gly Val Val Val Val Leu Thr Ser Arg Asp Gly Lys Arg Gly  
20 25 30

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Leu Gln Ala His Glu Asn Leu Ile Lys Ser Gly Ile Asn Pro Glu Asn  
35 40 45

ctt cac ttt cat cag ctc gat gtt act gac atc act agt att gct gct 193  
Leu His Phe His Gln Leu Asp Val Thr Asp Ile Thr Ser Ile Ala Ala  
50 55 60

att gct ggt ttc atc aat tcc aaa ttc ggc aaa ctt gat atc ctg gtg 241  
Ile Ala Gly Phe Ile Asn Ser Lys Phe Gly Lys Leu Asp Ile Leu Val  
65 70 75 80

aac aat gct gga att att gga gat atg gtt aac ttt gat gct tta ata 289  
Asn Asn Ala Gly Ile Ile Gly Asp Met Val Asn Phe Asp Ala Leu Ile  
85 90 95

gca gca gga ttt ggc act cca aga gaa cag atc aat ctt gag gac agt 337  
Ala Ala Gly Phe Gly Thr Pro Arg Glu Gln Ile Asn Leu Glu Asp Ser  
100 105 110

ccc ggg aca gta aca cag aca tat gag ctt acg aaa gaa tgc tta caa 385  
Pro Gly Thr Val Thr Gln Thr Tyr Glu Leu Thr Lys Glu Cys Leu Gln  
115 120 125

aca aat tat tat gga gcg aaa aga acc gtt gaa gct ttg ctt ccg ctt 433  
Thr Asn Tyr Tyr Gly Ala Lys Arg Thr Val Glu Ala Leu Leu Pro Leu  
130 135 140

ctc aag tta tcc gat tct cca agg att gtc aat gtc tcc tct ttt cta 481  
Leu Lys Leu Ser Asp Ser Pro Arg Ile Val Asn Val Ser Ser Phe Leu  
145 150 155 160

gga agg ttg acg tat ata cca aat gag acg atc aga ggg gtc cta aga 529  
Gly Arg Leu Thr Tyr Ile Pro Asn Glu Thr Ile Arg Gly Val Leu Arg  
165 170 175

gat gcc gag agc ctt aca gaa gaa cga ata gat gag att ctg aat gac	577																																																																				
Asp Ala Glu Ser Leu Thr Glu Glu Arg Ile Asp Glu Ile Leu Asn Asp																																																																					
180	185		190	atg ctg agg gac ttc aaa gac tgt tca ttc aaa gag aag gga tgg cct	625	Met Leu Arg Asp Phe Lys Asp Cys Ser Phe Lys Glu Lys Gly Trp Pro		195	200		205	aaa aat ctg gca gcc tat ata gtt tca aag gcg gcc ttg agt gca tac	673	Lys Asn Leu Ala Ala Tyr Ile Val Ser Lys Ala Ala Leu Ser Ala Tyr		210	215		220	aca aga ata ctg gct aag aaa tac cca tca atc atg atc aac tgt att	721	Thr Arg Ile Leu Ala Lys Lys Tyr Pro Ser Ile Met Ile Asn Cys Ile		225	230		235		240	tgc cct ggc ttt gtc aaa act gac atc aat gga aac aca gga cac ttg	769	Cys Pro Gly Phe Val Lys Thr Asp Ile Asn Gly Asn Thr Gly His Leu		245	250		255	ccg gtt gaa gaa ggt gca gcg agt ctg gca agg tta gcg ttg atg ccc	817	Pro Val Glu Glu Gly Ala Ala Ser Leu Ala Arg Leu Ala Leu Met Pro		260	265		270	caa att tta cct tct gga cta ttc ttt cag aga act gaa gtt tct tcg	865	Gln Ile Leu Pro Ser Gly Leu Phe Phe Gln Arg Thr Glu Val Ser Ser		275	280		285	ttt gaa taaaacaatt tgcctattca aaccaacacc acatatctat gaagtttcca	921	Phe Glu		290		ttttaggca tctttacgaa aaaaataaga catctgcaat actgttactg gaaaatgcaa	981	tgtactttt tcatgtatgc atggcgcagt tatttattct gactgcaaca ataagattct	1041	gttctttcaa ggcactctaa ggaatgctga tgtaccgttc tcaaacaagc agacaagtag	1101	acacgtttga ttgtcatgtc ttcattcgta caatcattt gtgtttgtat gttgagcatg	1161	tttaactaat tacaagagtg taattaagat caacttttat aaaaaaaaaa aaaaaaaaa	1219
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Met Leu Arg Asp Phe Lys Asp Cys Ser Phe Lys Glu Lys Gly Trp Pro																																																																					
195	200		205	aaa aat ctg gca gcc tat ata gtt tca aag gcg gcc ttg agt gca tac	673	Lys Asn Leu Ala Ala Tyr Ile Val Ser Lys Ala Ala Leu Ser Ala Tyr		210	215		220	aca aga ata ctg gct aag aaa tac cca tca atc atg atc aac tgt att	721	Thr Arg Ile Leu Ala Lys Lys Tyr Pro Ser Ile Met Ile Asn Cys Ile		225	230		235		240	tgc cct ggc ttt gtc aaa act gac atc aat gga aac aca gga cac ttg	769	Cys Pro Gly Phe Val Lys Thr Asp Ile Asn Gly Asn Thr Gly His Leu		245	250		255	ccg gtt gaa gaa ggt gca gcg agt ctg gca agg tta gcg ttg atg ccc	817	Pro Val Glu Glu Gly Ala Ala Ser Leu Ala Arg Leu Ala Leu Met Pro		260	265		270	caa att tta cct tct gga cta ttc ttt cag aga act gaa gtt tct tcg	865	Gln Ile Leu Pro Ser Gly Leu Phe Phe Gln Arg Thr Glu Val Ser Ser		275	280		285	ttt gaa taaaacaatt tgcctattca aaccaacacc acatatctat gaagtttcca	921	Phe Glu		290		ttttaggca tctttacgaa aaaaataaga catctgcaat actgttactg gaaaatgcaa	981	tgtactttt tcatgtatgc atggcgcagt tatttattct gactgcaaca ataagattct	1041	gttctttcaa ggcactctaa ggaatgctga tgtaccgttc tcaaacaagc agacaagtag	1101	acacgtttga ttgtcatgtc ttcattcgta caatcattt gtgtttgtat gttgagcatg	1161	tttaactaat tacaagagtg taattaagat caacttttat aaaaaaaaaa aaaaaaaaa	1219								
	205																																																																				
aaa aat ctg gca gcc tat ata gtt tca aag gcg gcc ttg agt gca tac	673																																																																				
Lys Asn Leu Ala Ala Tyr Ile Val Ser Lys Ala Ala Leu Ser Ala Tyr																																																																					
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	220																																																																				
aca aga ata ctg gct aag aaa tac cca tca atc atg atc aac tgt att	721																																																																				
Thr Arg Ile Leu Ala Lys Lys Tyr Pro Ser Ile Met Ile Asn Cys Ile																																																																					
225	230		235		240	tgc cct ggc ttt gtc aaa act gac atc aat gga aac aca gga cac ttg	769	Cys Pro Gly Phe Val Lys Thr Asp Ile Asn Gly Asn Thr Gly His Leu		245	250		255	ccg gtt gaa gaa ggt gca gcg agt ctg gca agg tta gcg ttg atg ccc	817	Pro Val Glu Glu Gly Ala Ala Ser Leu Ala Arg Leu Ala Leu Met Pro		260	265		270	caa att tta cct tct gga cta ttc ttt cag aga act gaa gtt tct tcg	865	Gln Ile Leu Pro Ser Gly Leu Phe Phe Gln Arg Thr Glu Val Ser Ser		275	280		285	ttt gaa taaaacaatt tgcctattca aaccaacacc acatatctat gaagtttcca	921	Phe Glu		290		ttttaggca tctttacgaa aaaaataaga catctgcaat actgttactg gaaaatgcaa	981	tgtactttt tcatgtatgc atggcgcagt tatttattct gactgcaaca ataagattct	1041	gttctttcaa ggcactctaa ggaatgctga tgtaccgttc tcaaacaagc agacaagtag	1101	acacgtttga ttgtcatgtc ttcattcgta caatcattt gtgtttgtat gttgagcatg	1161	tttaactaat tacaagagtg taattaagat caacttttat aaaaaaaaaa aaaaaaaaa	1219																								
	235		240	tgc cct ggc ttt gtc aaa act gac atc aat gga aac aca gga cac ttg	769	Cys Pro Gly Phe Val Lys Thr Asp Ile Asn Gly Asn Thr Gly His Leu		245	250		255	ccg gtt gaa gaa ggt gca gcg agt ctg gca agg tta gcg ttg atg ccc	817	Pro Val Glu Glu Gly Ala Ala Ser Leu Ala Arg Leu Ala Leu Met Pro		260	265		270	caa att tta cct tct gga cta ttc ttt cag aga act gaa gtt tct tcg	865	Gln Ile Leu Pro Ser Gly Leu Phe Phe Gln Arg Thr Glu Val Ser Ser		275	280		285	ttt gaa taaaacaatt tgcctattca aaccaacacc acatatctat gaagtttcca	921	Phe Glu		290		ttttaggca tctttacgaa aaaaataaga catctgcaat actgttactg gaaaatgcaa	981	tgtactttt tcatgtatgc atggcgcagt tatttattct gactgcaaca ataagattct	1041	gttctttcaa ggcactctaa ggaatgctga tgtaccgttc tcaaacaagc agacaagtag	1101	acacgtttga ttgtcatgtc ttcattcgta caatcattt gtgtttgtat gttgagcatg	1161	tttaactaat tacaagagtg taattaagat caacttttat aaaaaaaaaa aaaaaaaaa	1219																										
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tgc cct ggc ttt gtc aaa act gac atc aat gga aac aca gga cac ttg	769																																																																				
Cys Pro Gly Phe Val Lys Thr Asp Ile Asn Gly Asn Thr Gly His Leu																																																																					
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	255																																																																				
ccg gtt gaa gaa ggt gca gcg agt ctg gca agg tta gcg ttg atg ccc	817																																																																				
Pro Val Glu Glu Gly Ala Ala Ser Leu Ala Arg Leu Ala Leu Met Pro																																																																					
260	265		270	caa att tta cct tct gga cta ttc ttt cag aga act gaa gtt tct tcg	865	Gln Ile Leu Pro Ser Gly Leu Phe Phe Gln Arg Thr Glu Val Ser Ser		275	280		285	ttt gaa taaaacaatt tgcctattca aaccaacacc acatatctat gaagtttcca	921	Phe Glu		290		ttttaggca tctttacgaa aaaaataaga catctgcaat actgttactg gaaaatgcaa	981	tgtactttt tcatgtatgc atggcgcagt tatttattct gactgcaaca ataagattct	1041	gttctttcaa ggcactctaa ggaatgctga tgtaccgttc tcaaacaagc agacaagtag	1101	acacgtttga ttgtcatgtc ttcattcgta caatcattt gtgtttgtat gttgagcatg	1161	tttaactaat tacaagagtg taattaagat caacttttat aaaaaaaaaa aaaaaaaaa	1219																																										
	270																																																																				
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Gln Ile Leu Pro Ser Gly Leu Phe Phe Gln Arg Thr Glu Val Ser Ser																																																																					
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	285																																																																				
ttt gaa taaaacaatt tgcctattca aaccaacacc acatatctat gaagtttcca	921																																																																				
Phe Glu																																																																					
290																																																																					
ttttaggca tctttacgaa aaaaataaga catctgcaat actgttactg gaaaatgcaa	981																																																																				
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<210> 52  
<211> 290  
<212> PRT  
<213> Sueada japonica

<400> 52																	
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	10																
	15																
Ala Lys Gly Val Val Val Val Leu Thr Ser Arg Asp Gly Lys Arg Gly																	
20	25		30	Leu Gln Ala His Glu Asn Leu Ile Lys Ser Gly Ile Asn Pro Glu Asn		35	40		45								
	30																
Leu Gln Ala His Glu Asn Leu Ile Lys Ser Gly Ile Asn Pro Glu Asn																	
35	40		45														
	45																

Leu His Phe His Gln Leu Asp Val Thr Asp Ile Thr Ser Ile Ala Ala  
50 55 60

Ile Ala Gly Phe Ile Asn Ser Lys Phe Gly Lys Leu Asp Ile Leu Val  
65 70 75 80

Asn Asn Ala Gly Ile Ile Gly Asp Met Val Asn Phe Asp Ala Leu Ile  
85 90 95

Ala Ala Gly Phe Gly Thr Pro Arg Glu Gln Ile Asn Leu Glu Asp Ser  
100 105 110

Pro Gly Thr Val Thr Gln Thr Tyr Glu Leu Thr Lys Glu Cys Leu Gln  
115 120 125

Thr Asn Tyr Tyr Gly Ala Lys Arg Thr Val Glu Ala Leu Leu Pro Leu  
130 135 140

Leu Lys Leu Ser Asp Ser Pro Arg Ile Val Asn Val Ser Ser Phe Leu  
145 150 155 160

Gly Arg Leu Thr Tyr Ile Pro Asn Glu Thr Ile Arg Gly Val Leu Arg  
165 170 175

Asp Ala Glu Ser Leu Thr Glu Glu Arg Ile Asp Glu Ile Leu Asn Asp  
180 185 190

Met Leu Arg Asp Phe Lys Asp Cys Ser Phe Lys Glu Lys Gly Trp Pro  
195 200 205

Lys Asn Leu Ala Ala Tyr Ile Val Ser Lys Ala Ala Leu Ser Ala Tyr  
210 215 220

Thr Arg Ile Leu Ala Lys Lys Tyr Pro Ser Ile Met Ile Asn Cys Ile  
225 230 235 240

Cys Pro Gly Phe Val Lys Thr Asp Ile Asn Gly Asn Thr Gly His Leu  
245 250 255

Pro Val Glu Glu Gly Ala Ala Ser Leu Ala Arg Leu Ala Leu Met Pro  
260 265 270

Gln Ile Leu Pro Ser Gly Leu Phe Phe Gln Arg Thr Glu Val Ser Ser  
275 280 285

Phe Glu  
290

<210> 53  
<211> 1148  
<212> DNA  
<213> Sueada japonica

<220>

<221> CDS

<222> (3)..(848)

<400> 53

ga agc agg ccg gat atc cat gtt gaa caa gct cat tca gat gat att 47  
Ser Arg Pro Asp Ile His Val Glu Gln Ala His Ser Asp Asp Ile  
1 5 10 15

act ggg ttg aaa ttc tca tgt gat ggt cgt cat ctg ttg tct aga agt 95  
Thr Gly Leu Lys Phe Ser Cys Asp Gly Arg His Leu Leu Ser Arg Ser  
20 25 30

ttt gat tgc aca ctt aag gtt tgg gac ttg cgc caa atg aag cgg tct 143  
Phe Asp Cys Thr Leu Lys Val Trp Asp Leu Arg Gln Met Lys Arg Ser  
35 40 45

ctt aag gtg ttt gat gaa tta cca aat cac tat gct caa acg aat gtc 191  
Leu Lys Val Phe Asp Glu Leu Pro Asn His Tyr Ala Gln Thr Asn Val  
50 55 60

tca ttt agt cca gat gag cag ctc atc ttg act ggt aca tct gta gaa 239  
Ser Phe Ser Pro Asp Glu Gln Leu Ile Leu Thr Gly Thr Ser Val Glu  
65 70 75

agg gat agc cca act gga gga ttg ttg tgc ttt tat gat cgg gaa aaa 287  
Arg Asp Ser Pro Thr Gly Gly Leu Leu Cys Phe Tyr Asp Arg Glu Lys  
80 85 90 95

ctt gaa cta gta tca aaa gtt ggc att tct cct act tgc agt gtt gtg 335  
Leu Glu Leu Val Ser Lys Val Gly Ile Ser Pro Thr Cys Ser Val Val  
100 105 110

caa tgt gcc tgg cac cca agg ctg aat cag gtt ttt gcc act gct gga 383  
Gln Cys Ala Trp His Pro Arg Leu Asn Gln Val Phe Ala Thr Ala Gly  
115 120 125

aat aaa agc caa gga ggt aca cat gta ctc tat gat cca acc atg agt 431  
Asn Lys Ser Gln Gly Gly Thr His Val Leu Tyr Asp Pro Thr Met Ser  
130 135 140

gag aga ggt gct ctt gtg tgt gtt gct cgt gca cca agg atg aaa tca 479  
Glu Arg Gly Ala Leu Val Cys Val Ala Arg Ala Pro Arg Met Lys Ser  
145 150 155

gtg gat gat ttt gag gtg cag ccg gtt ata cat aac cct cac gca ctt 527  
Val Asp Asp Phe Glu Val Gln Pro Val Ile His Asn Pro His Ala Leu  
160 165 170 175

ccc ttg ttc aga gat cag cca agc cgc aaa cgt caa aga gag aag att 575  
Pro Leu Phe Arg Asp Gln Pro Ser Arg Lys Arg Gln Arg Glu Lys Ile  
180 185 190

ctg aag gac cca ata aaa tcc cac aaa cca gag ctt cct atg tca gga 623  
Leu Lys Asp Pro Ile Lys Ser His Lys Pro Glu Leu Pro Met Ser Gly  
195 200 205

cct ggc cat ggt ggc aga act ggt aca tca tcg ggt agt ttg tta aca 671



Cys Ala Trp His Pro Arg Leu Asn Gln Val Phe Ala Thr Ala Gly Asn  
 115 120 125  
 Lys Ser Gln Gly Gly Thr His Val Leu Tyr Asp Pro Thr Met Ser Glu  
 130 135 140  
 Arg Gly Ala Leu Val Cys Val Ala Arg Ala Pro Arg Met Lys Ser Val  
 145 150 155 160  
 Asp Asp Phe Glu Val Gln Pro Val Ile His Asn Pro His Ala Leu Pro  
 165 170 175  
 Leu Phe Arg Asp Gln Pro Ser Arg Lys Arg Gln Arg Glu Lys Ile Leu  
 180 185 190  
 Lys Asp Pro Ile Lys Ser His Lys Pro Glu Leu Pro Met Ser Gly Pro  
 195 200 205  
 Gly His Gly Gly Arg Thr Gly Thr Ser Ser Gly Ser Leu Leu Thr Gln  
 210 215 220  
 Tyr Leu Leu Lys Gln Gly Gly Met Leu Lys Glu Thr Trp Met Asp Glu  
 225 230 235 240  
 Asp Pro Arg Glu Ala Ile Leu Lys Tyr Ala Asp Ala Ala Glu Lys Asp  
 245 250 255  
 Pro Lys Phe Ile Ala Pro Ala Tyr Ala Glu Thr Gln Pro Lys Pro Val  
 260 265 270  
 Phe Glu Asp Ser Asp Lys Glu Asp Glu Glu  
 275 280

<210> 55  
 <211> 1193  
 <212> DNA  
 <213> Avicennia marina

<220>  
 <221> CDS  
 <222> (3)..(815)

<400> 55  
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 Ala Pro Glu Leu Leu Gly Ala Lys His Tyr Thr Ser Ala Val  
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 gac atg tgg gct gtg ggc tgc att ttt gct gag ctt ctg act cta aag 95  
 Asp Met Trp Ala Val Gly Cys Ile Phe Ala Glu Leu Leu Thr Leu Lys  
 20 25 30  
 cca cta ttt caa ggg caa gaa gta aaa ggg act tct aat cca ttt cag 143  
 Pro Leu Phe Gln Gly Gln Glu Val Lys Gly Thr Ser Asn Pro Phe Gln  
 35 40 45

ctt gat caa ctt gac aaa atc ttt aag gtc cta ggt cat ccc acg caa	191		
Leu Asp Gln Leu Asp Lys Ile Phe Lys Val Leu Gly His Pro Thr Gln			
50	55	60	
gaa aag tgg ccc aca cta gcg aat ctt cca cat tgg cag tct gat gtg	239		
Glu Lys Trp Pro Thr Leu Ala Asn Leu Pro His Trp Gln Ser Asp Val			
65	70	75	
caa cgt atc caa ggg ctc aaa tac gac aat act gga ctt tac aat gtt	287		
Gln Arg Ile Gln Gly Leu Lys Tyr Asp Asn Thr Gly Leu Tyr Asn Val			
80	85	90	95
gtt cat ctc tcc ccc aaa aat cca gca tat gac ctt ctc tca aag atg	335		
Val His Leu Ser Pro Lys Asn Pro Ala Tyr Asp Leu Leu Ser Lys Met			
100	105	110	
ctt gag tat gat cct aga aaa aga ata aca gct aca caa gct ctt gag	383		
Leu Glu Tyr Asp Pro Arg Lys Arg Ile Thr Ala Thr Gln Ala Leu Glu			
115	120	125	
cat gag tat ttt cgc atg gaa cct ttg ccg gga cgc aac gct ctg gta	431		
His Glu Tyr Phe Arg Met Glu Pro Leu Pro Gly Arg Asn Ala Leu Val			
130	135	140	
cca cca cag cct ggg gag aaa att gtg aac tac cca aca cga cca gtg	479		
Pro Pro Gln Pro Gly Glu Lys Ile Val Asn Tyr Pro Thr Arg Pro Val			
145	150	155	
gac aca aat act gat att gaa gga aca atc agc ctc cag ccc tct caa	527		
Asp Thr Asn Thr Asp Ile Glu Gly Thr Ile Ser Leu Gln Pro Ser Gln			
160	165	170	175
ccg gta tca tct ggg aat tct gtg tct ggg gcc cta gcc ggt cct cat	575		
Pro Val Ser Ser Gly Asn Ser Val Ser Gly Ala Leu Ala Gly Pro His			
180	185	190	
gta atg caa aat aga tcc atg cct cgg cca atg ccc atg gtt ggc gtg	623		
Val Met Gln Asn Arg Ser Met Pro Arg Pro Met Pro Met Val Gly Val			
195	200	205	
caa cgc atg caa cct cca ggg atc cca cac tat ggt ctt gct tct cag	671		
Gln Arg Met Gln Pro Pro Gly Ile Pro His Tyr Gly Leu Ala Ser Gln			
210	215	220	
gca gga atg ggt gga gta aat cct ggt ggc atc cca att cag cgg gga	719		
Ala Gly Met Gly Gly Val Asn Pro Gly Gly Ile Pro Ile Gln Arg Gly			
225	230	235	
gtt cct gct cag gct cat caa cag cag cag atg aga agg aaa gac cct	767		
Val Pro Ala Gln Ala His Gln Gln Gln Met Arg Arg Lys Asp Pro			
240	245	250	255
gga atg ggg atg act gga tat cct cca caa cag aaa tca agg cgc ttt	815		
Gly Met Gly Met Thr Gly Tyr Pro Pro Gln Gln Lys Ser Arg Arg Phe			
260	265	270	
tgagagtccg ggtggatttg gagcctaagt gggaggacaa atacacattc caatcaaatt	875		

agaggaaacc ttaaattaaat cttccagtca gctgaaacga caccagtgga accaaatgtat 935  
ctgaccat ttccaggatt gcatgtattt attaggagga atacacgaat gaagattcga 995  
gtctagtgcc aaattattct aacatacctt catcatttgt tcctactaca ttccgacgtt 1055  
atatgttca actagtggaa gggtttctgc agtccaccca tgtggcacaa acatgattca 1115  
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<210> 56  
<211> 271  
<212> PRT  
<213> Avicennia marina

<400> 56  
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Leu Phe Gln Gly Gln Glu Val Lys Gly Thr Ser Asn Pro Phe Gln Leu  
35 40 45  
Asp Gln Leu Asp Lys Ile Phe Lys Val Leu Gly His Pro Thr Gln Glu  
50 55 60  
Lys Trp Pro Thr Leu Ala Asn Leu Pro His Trp Gln Ser Asp Val Gln  
65 70 75 80  
Arg Ile Gln Gly Leu Lys Tyr Asp Asn Thr Gly Leu Tyr Asn Val Val  
85 90 95  
His Leu Ser Pro Lys Asn Pro Ala Tyr Asp Leu Leu Ser Lys Met Leu  
100 105 110  
Glu Tyr Asp Pro Arg Lys Arg Ile Thr Ala Thr Gln Ala Leu Glu His  
115 120 125  
Glu Tyr Phe Arg Met Glu Pro Leu Pro Gly Arg Asn Ala Leu Val Pro  
130 135 140  
Pro Gln Pro Gly Glu Lys Ile Val Asn Tyr Pro Thr Arg Pro Val Asp  
145 150 155 160  
Thr Asn Thr Asp Ile Glu Gly Thr Ile Ser Leu Gln Pro Ser Gln Pro  
165 170 175  
Val Ser Ser Gly Asn Ser Val Ser Gly Ala Leu Ala Gly Pro His Val  
180 185 190  
Met Gln Asn Arg Ser Met Pro Arg Pro Met Pro Met Val Gly Val Gln

195	200	205
Arg Met Gln Pro Pro Gly Ile Pro His Tyr Gly Leu Ala Ser Gln Ala		
210	215	220
Gly Met Gly Gly Val Asn Pro Gly Gly Ile Pro Ile Gln Arg Gly Val		
225	230	235
240		
Pro Ala Gln Ala His Gln Gln Gln Met Arg Arg Lys Asp Pro Gly		
245	250	255
Met Gly Met Thr Gly Tyr Pro Pro Gln Gln Lys Ser Arg Arg Phe		
260	265	270
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<211> 1195		
<212> DNA		
<213> Sueada japonica		
<220>		
<221> CDS		
<222> (116)..(1195)		
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atagtggcaa aacaatagag ggcaaattct cattgccaa ttcaaatttg gtaaa atg 118		
Met		
1		
gct caa aag cat ttg aaa gaa ctt ctc aaa gaa gat caa gaa ccc ttt 166		
Ala Gln His Leu Lys Glu Leu Leu Lys Glu Asp Gln Glu Pro Phe		
5	10	15
cat tta aag gat tac att gca act aaa aaa tgt caa ctt ttg aag aag 214		
His Leu Lys Asp Tyr Ile Ala Thr Lys Lys Cys Gln Leu Leu Lys Lys		
20	25	30
caa gaa tta gta gta ccc aaa tca aaa ctt caa ctc aaa aag cca aag 262		
Gln Glu Leu Val Val Pro Lys Ser Lys Leu Gln Leu Lys Lys Pro Lys		
35	40	45
cca aaa cca att tca aaa agc act tca gtt ttg tgc aaa aat gct tgc 310		
Pro Lys Pro Ile Ser Lys Ser Thr Ser Val Leu Cys Lys Asn Ala Cys		
50	55	60
65		
ttt tta tct tta caa gaa tcc cct gac ctc aga aaa tcc ccc aaa cta 358		
Phe Leu Ser Leu Gln Glu Ser Pro Asp Leu Arg Lys Ser Pro Lys Leu		
70	75	80
ttt gat ttt cca cct tcc cct gtt tct aac aaa agc cca aac aga gta 406		
Phe Asp Phe Pro Pro Ser Pro Val Ser Asn Lys Ser Pro Asn Arg Val		
85	90	95
ttc ctc aat gtt cct gct aaa act gct gct ctt ctt gaa gct gct 454		

Phe	Leu	Asn	Val	Pro	Ala	Lys	Thr	Ala	Ala	Leu	Leu	Leu	Glu	Ala	Ala	
100							105						110			
att	cga	att	caa	acc	cac	aaa	tct	aaa	ccc	aaa	acc	cag	att	aaa	aat	502
Ile	Arg	Ile	Gln	Thr	His	Lys	Ser	Lys	Pro	Lys	Thr	Gln	Ile	Lys	Asn	
115							120					125				
tcg	ggt	ttt	ggg	cta	ttc	ggg	tca	atg	tta	aag	cga	tta	aat	ctt	cga	550
Ser	Gly	Phe	Gly	Leu	Phe	Gly	Ser	Met	Leu	Lys	Arg	Leu	Asn	Leu	Arg	
130							135				140		145			
aat	cgt	acc	caa	aaa	atc	aag	tca	aaa	aca	gag	gaa	caa	aac	aga	gga	598
Asn	Arg	Thr	Gln	Lys	Ile	Lys	Ser	Lys	Thr	Glu	Glu	Gln	Asn	Arg	Gly	
							150			155		160				
tgc	tct	gtt	ttg	agg	agt	gtt	gaa	gaa	aaa	act	acc	acc	att	tct	646	
Cys	Ser	Val	Leu	Arg	Ser	Val	Glu	Glu	Glu	lys	lys	lys	lys	lys		
							165			170		175				
tct	tct	tca	tct	tct	tca	aca	tca	tcg	tat	tct	tcg	tgt	tct		694	
Ser	Thr	Ser	Ser	Tyr	Ser	Ser	Cys	Ser								
							180			185		190				
tgc	aat	gag	agg	tta	agt	agt	ttg	gat	ttg	gag	agt	tct	agc	agt	gga	742
Cys	Asn	Glu	Arg	Leu	Ser	Ser	Leu	Asp	Leu	Glu	Ser	Ser	Ser	Ser	Gly	
							195			200		205				
aga	tca	tta	cat	gat	gaa	gat	gaa	gat	gaa	gat	gat	gaa	ttt		790	
Arg	Ser	Leu	His	Asp	Glu	Asp	Glu	Asp	Glu	Asp	Asp	Asp	Glu	Phe		
							210			215		220		225		
gag	ttt	aca	aat	gtt	tta	aga	gaa	aat	aat	gat	gat	aaa	aat	gga		838
Glu	Phe	Thr	Asn	Val	Leu	Arg	Glu	Asn	Asn	Asn	Asn	Asp	Asp	Lys	Asn	Gly
							230			235		240				
ggt	tat	tat	tca	gga	att	tgc	tta	agt	cct	ttg	agt	cca	ttt	cgt	ttt	886
Gly	Tyr	Tyr	Ser	Gly	Ile	Cys	Leu	Ser	Pro	Leu	Ser	Pro	Phe	Arg	Phe	
							245			250		255				
gct	ctt	cat	aaa	aac	tct	tct	cct	gaa	cgt	tgc	tct	cct	gct	aaa	tcc	934
Ala	Leu	His	Lys	Asn	Ser	Ser	Pro	Glu	Arg	Cys	Ser	Pro	Ala	Lys	Ser	
							260			265		270				
cct	gtt	cgt	tgc	aaa	ttt	gag	ggt	aat	gct	aaa	tat	gaa	caa	gaa	agc	982
Pro	Val	Arg	Cys	Lys	Phe	Glu	Gly	Asn	Ala	Lys	Tyr	Glu	Gln	Glu	Ser	
							275			280		285				
tta	ata	aag	ttt	gaa	gac	gaa	gat	gaa	gac	aaa	gag	caa	aat	agc		1030
Leu	Ile	Lys	Phe	Glu	Asp	Glu	Asp	Glu	Asp	Lys	Glu	Gln	Asn	Ser		
							290			295		300		305		
cct	gtt	tcc	gtg	ctc	gat	cct	cca	ttc	gag	gat	gat	tac	gat	ggg	cat	1078
Pro	Val	Ser	Val	Leu	Asp	Pro	Pro	Phe	Glu	Asp	Asp	Tyr	Asp	Gly	His	
								310			315		320			
gag	gag	gat	agc	tac	gag	gac	atc	gaa	tgc	agc	tat	gct	ttt	gta	caa	1126
Glu	Glu	Asp	Ser	Tyr	Glu	Asp	Ile	Glu	Cys	Ser	Tyr	Ala	Phe	Val	Gln	

325

330

335

aga gca caa caa gag tta ttg cac aga ctt cac cgg ttc cag aag cta 1174  
 Arg Ala Gln Gln Glu Leu Leu His Arg Leu His Arg Phe Gln Lys Leu  
 340 345 350

gcg gag ttg gac cca att gaa 1195  
 Ala Glu Leu Asp Pro Ile Glu  
 355 360

<210> 58  
 <211> 360  
 <212> PRT  
 <213> Sueada japonica

<400> 58  
 Met Ala Gln Lys His Leu Lys Glu Leu Leu Lys Glu Asp Gln Glu Pro  
 1 5 10 15

Phe His Leu Lys Asp Tyr Ile Ala Thr Lys Lys Cys Gln Leu Leu Lys  
 20 25 30

Lys Gln Glu Leu Val Val Pro Lys Ser Lys Leu Gln Leu Lys Lys Pro  
 35 40 45

Lys Pro Lys Pro Ile Ser Lys Ser Thr Ser Val Leu Cys Lys Asn Ala  
 50 55 60

Cys Phe Leu Ser Leu Gln Glu Ser Pro Asp Leu Arg Lys Ser Pro Lys  
 65 70 75 80

Leu Phe Asp Phe Pro Pro Ser Pro Val Ser Asn Lys Ser Pro Asn Arg  
 85 90 95

Val Phe Leu Asn Val Pro Ala Lys Thr Ala Ala Leu Leu Leu Glu Ala  
 100 105 110

Ala Ile Arg Ile Gln Thr His Lys Ser Lys Pro Lys Thr Gln Ile Lys  
 115 120 125

Asn Ser Gly Phe Gly Leu Phe Gly Ser Met Leu Lys Arg Leu Asn Leu  
 130 135 140

Arg Asn Arg Thr Gln Lys Ile Lys Ser Lys Thr Glu Glu Gln Asn Arg  
 145 150 155 160

Gly Cys Ser Val Leu Arg Ser Val Glu Glu Glu Lys Thr Thr Thr Ile  
 165 170 175

Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Tyr Ser Ser Cys  
 180 185 190

Ser Cys Asn Glu Arg Leu Ser Ser Leu Asp Leu Glu Ser Ser Ser Ser  
 195 200 205

Gly Arg Ser Leu His Asp Glu Asp Glu Asp Glu Asp Asp Glu

210	215	220	
Phe Glu Phe Thr Asn Val Leu Arg Glu Asn Asn Asn Asp Asp Lys Asn			
225	230	235	240
Gly Gly Tyr Tyr Ser Gly Ile Cys Leu Ser Pro Leu Ser Pro Phe Arg			
245	250	255	
Phe Ala Leu His Lys Asn Ser Ser Pro Glu Arg Cys Ser Pro Ala Lys			
260	265	270	
Ser Pro Val Arg Cys Lys Phe Glu Gly Asn Ala Lys Tyr Glu Gln Glu			
275	280	285	
Ser Leu Ile Lys Phe Glu Asp Glu Asp Glu Asp Lys Glu Gln Asn			
290	295	300	
Ser Pro Val Ser Val Leu Asp Pro Pro Phe Glu Asp Asp Tyr Asp Gly			
305	310	315	320
His Glu Glu Asp Ser Tyr Glu Asp Ile Glu Cys Ser Tyr Ala Phe Val			
325	330	335	
Gln Arg Ala Gln Gln Glu Leu Leu His Arg Leu His Arg Phe Gln Lys			
340	345	350	
Leu Ala Glu Leu Asp Pro Ile Glu			
355	360		
<210> 59			
<211> 1301			
<212> DNA			
<213> Salsola komarovii			
<220>			
<221> CDS			
<222> (3)...(815)			
<400> 59			
gt gag gtt gac gat agc gtt aat agt cta cag gca gat gtt gac aac			47
Glu Val Asp Asp Ser Val Asn Ser Leu Gln Ala Asp Val Asp Asn			
1	5	10	15
ctt tca att gag gaa cgc aga ttg gat gaa cag ata agg gaa atg caa			95
Leu Ser Ile Glu Glu Arg Arg Leu Asp Glu Gln Ile Arg Glu Met Gln			
20	25	30	
gaa aga ttg agg gaa atg agt gaa gat gat atc aat cag aag tgg ctt			143
Glu Arg Leu Arg Glu Met Ser Glu Asp Asp Ile Asn Gln Lys Trp Leu			
35	40	45	
ttt gta act gaa gaa gac ata aag ggt tta cct tgt ttt cag aat gaa			191
Phe Val Thr Glu Glu Asp Ile Lys Gly Leu Pro Cys Phe Gln Asn Glu			
50	55	60	

acc tta att gca att aaa gct cca cat gga aca act ttg gag gtt cca 239  
 Thr Leu Ile Ala Ile Lys Ala Pro His Gly Thr Thr Leu Glu Val Pro  
 65 70 75

gat cca gat gag gct gtc gat tat cct caa aga aga tac aag ata gtt 287  
 Asp Pro Asp Glu Ala Val Asp Tyr Pro Gln Arg Arg Tyr Lys Ile Val  
 80 85 90 95

ctt agg agc aca atg ggt cct att gat gta tat tta gtc agt caa ttt 335  
 Leu Arg Ser Thr Met Gly Pro Ile Asp Val Tyr Leu Val Ser Gln Phe  
 100 105 110

gaa gag aag ttt gag gag atc agt ggt gct gac ggt cca cta agt ata 383  
 Glu Glu Lys Phe Glu Glu Ile Ser Gly Ala Asp Gly Pro Leu Ser Ile  
 115 120 125

cca agt acc tca ggt gat gac aaa cac aca act gtt gca gct aag gaa 431  
 Pro Ser Thr Ser Gly Asp Asp Lys His Thr Thr Val Ala Ala Lys Glu  
 130 135 140

gaa agc aat ggc aat gag att gaa ata gaa gga caa ggg acc cat aga 479  
 Glu Ser Asn Gly Asn Glu Ile Glu Ile Glu Gly Gln Gly Thr His Arg  
 145 150 155

atc tgc tca gat tcc aac gct cag caa gac ttt gtg agt gga att atg 527  
 Ile Cys Ser Asp Ser Asn Ala Gln Gln Asp Phe Val Ser Gly Ile Met  
 160 165 170 175

aag ata gtg cct gaa gtt gat agt gat gca gat tac tgg ttg cta tcg 575  
 Lys Ile Val Pro Glu Val Asp Ser Asp Ala Asp Tyr Trp Leu Leu Ser  
 180 185 190

gat gct gat gtt agc att act gac atg tgg gga act gat tct gga gtt 623  
 Asp Ala Asp Val Ser Ile Thr Asp Met Trp Gly Thr Asp Ser Gly Val  
 195 200 205

gaa tgg aat gaa tta ggg act ata cat gaa gac tat gcc gtg gct aat 671  
 Glu Trp Asn Glu Leu Gly Thr Ile His Glu Asp Tyr Ala Val Ala Asn  
 210 215 220

gtt ggc act tca cag cca caa agt cca cca aca agt gca aca gaa gtg 719  
 Val Gly Thr Ser Gln Pro Gln Ser Pro Pro Thr Ser Ala Thr Glu Val  
 225 230 235

ctt cca gct aac atg aca agc agg aga ttg aca tgg agt ttt gag aga 767  
 Leu Pro Ala Asn Met Thr Ser Arg Arg Leu Thr Trp Ser Phe Glu Arg  
 240 245 250 255

att gcc aar att cat tca aat ggt cac tat tgc ttg gaa gtg agg ctc 815  
 Ile Ala Lys Ile His Ser Asn Gly His Tyr Cys Leu Glu Val Arg Leu  
 260 265 270

taactttcta ttattcatcc tgggatttgg gtacgaaagt ctgccttgaa gatgctgtaa 875

catgttgtgt attacaactg tgtgaatcta gtaagttggt agggtgagat tgttcctgat 935

cttattgcac agccgggttgg gagagattga tcgctcaaca actgacaaaa ttggggcatg 995

ttaacggata gtagcagtt gtaattttgt acatcacatt tgttgatttt agtcagtaca 1055  
tcataactag ctcttcctat acttcttcaa ttgtcaactg gaatagattt ttagattaat 1115  
tagatctctc tttgtatgga aatgtttcag ggtaacaagc cagaaattaa aatggttta 1175  
tgtgtaaaaa tatatactta aattgtttgt aggaagttc tgatgggttg ttggatggct 1235  
tttaacaact acatcgata aggaaattcg tattcacaat tcacaatgaa aaaaaaaaaa 1295  
aaaaaaaaa 1301

<210> 60  
<211> 271  
<212> PRT  
<213> Salsola komarovii

<400> 60  
Glu Val Asp Asp Ser Val Asn Ser Leu Gln Ala Asp Val Asp Asn Leu  
1 5 10 15  
Ser Ile Glu Glu Arg Arg Leu Asp Glu Gln Ile Arg Glu Met Gln Glu  
20 25 30  
Arg Leu Arg Glu Met Ser Glu Asp Asp Ile Asn Gln Lys Trp Leu Phe  
35 40 45  
Val Thr Glu Glu Asp Ile Lys Gly Leu Pro Cys Phe Gln Asn Glu Thr  
50 55 60  
Leu Ile Ala Ile Lys Ala Pro His Gly Thr Thr Leu Glu Val Pro Asp  
65 70 75 80  
Pro Asp Glu Ala Val Asp Tyr Pro Gln Arg Arg Tyr Lys Ile Val Leu  
85 90 95  
Arg Ser Thr Met Gly Pro Ile Asp Val Tyr Leu Val Ser Gln Phe Glu  
100 105 110  
Glu Lys Phe Glu Glu Ile Ser Gly Ala Asp Gly Pro Leu Ser Ile Pro  
115 120 125  
Ser Thr Ser Gly Asp Asp Lys His Thr Thr Val Ala Ala Lys Glu Glu  
130 135 140  
Ser Asn Gly Asn Glu Ile Glu Ile Glu Gly Gln Gly Thr His Arg Ile  
145 150 155 160  
Cys Ser Asp Ser Asn Ala Gln Gln Asp Phe Val Ser Gly Ile Met Lys  
165 170 175  
Ile Val Pro Glu Val Asp Ser Asp Ala Asp Tyr Trp Leu Leu Ser Asp  
180 185 190  
Ala Asp Val Ser Ile Thr Asp Met Trp Gly Thr Asp Ser Gly Val Glu

195

200

205

Trp Asn Glu Leu Gly Thr Ile His Glu Asp Tyr Ala Val Ala Asn Val  
 210 215 220

Gly Thr Ser Gln Pro Gln Ser Pro Pro Thr Ser Ala Thr Glu Val Leu  
 225 230 235 240

Pro Ala Asn Met Thr Ser Arg Arg Leu Thr Trp Ser Phe Glu Arg Ile  
 245 250 255

Ala Lys Ile His Ser Asn Gly His Tyr Cys Leu Glu Val Arg Leu  
 260 265 270

&lt;210&gt; 61

&lt;211&gt; 1032

&lt;212&gt; DNA

&lt;213&gt; Salsola komarovii

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(732)

&lt;400&gt; 61

cca caa cga aga ccc gac ccg gtc ccg aac ctt cac ggt cag ctt ttt 48  
 Pro Gln Arg Arg Pro Asp Pro Val Pro Asn Leu His Gly Gln Leu Phe  
 1 5 10 15

caa cac cga aat cca cac cac cgt gac ctc cac ccc tgc cgt agc ccg 96  
 Gln His Arg Asn Pro His His Arg Asp Leu His Pro Cys Arg Ser Pro  
 20 25 30

gca atg ggt cca ctc cct ccg cag act cat ctg cgc tgg tat tcc ctc 144  
 Ala Met Gly Pro Leu Pro Pro Gln Thr His Leu Arg Trp Tyr Ser Leu  
 35 40 45

tcg cgc tac tcc ccc gtg atc ggc ctc ggc gtc caa tgg aag ccc tcc 192  
 Ser Arg Tyr Ser Pro Val Ile Gly Leu Gly Val Gln Trp Lys Pro Ser  
 50 55 60

tcc acc tca gct gcc act ctt caa ctc agc atc gac aaa aag tgc ctc 240  
 Ser Thr Ser Ala Ala Thr Leu Gln Leu Ser Ile Asp Lys Lys Cys Leu  
 65 70 75 80

atc ttc caa ctc tcc cac tcc ccc gcc atc ccc gcc acc ctc cgc gac 288  
 Ile Phe Gln Leu Ser His Ser Pro Ala Ile Pro Ala Thr Leu Arg Asp  
 85 90 95

ctc ctc ctc gac gat cgc gtc acc ttc ttt ggt gtc cac aac ggc cgt 336  
 Leu Leu Leu Asp Asp Arg Val Thr Phe Phe Gly Val His Asn Gly Arg  
 100 105 110

gcc cgc gac ctc ctc caa ggg tcc cac cat gag ctc gac gtc aac aat 384  
 Ala Arg Asp Leu Leu Gln Gly Ser His His Glu Leu Asp Val Asn Asn  
 115 120 125

ctg gtt gat ctt gcc gag gag gaa aat ggt cat tac ttg aag tgg tcc	432
Leu Val Asp Leu Ala Glu Glu Glu Asn Gly His Tyr Leu Lys Trp Ser	
130 135 140	
atg gaa gac atg gct gaa gat gtg ttg ggc ttt tgg gta cac aaa	480
Met Glu Asp Met Ala Glu Asp Val Leu Gly Phe Cys Gly Val His Lys	
145 150 155 160	
ccc agg aag gtt atg tta agt ggt tgg gat cag tat tgc ttg tct aat	528
Pro Arg Lys Val Met Leu Ser Gly Trp Asp Gln Tyr Cys Leu Ser Asn	
165 170 175	
gac cag gtt cag tat gct tgg gat gct tac gtt tct ctt cgt ctt	576
Asp Gln Val Gln Tyr Ala Cys Val Asp Ala Tyr Val Ser Leu Arg Leu	
180 185 190	
gct cga gct tat ggg tac cac cgt ctc gat cac gat gat tat gat	624
Ala Arg Ala Tyr Gly Tyr His Arg Leu Asp His Asp Asp Asp Tyr Asp	
195 200 205	
gac cat gac gac gat gat aac gac cac acc gat gat tac gat gac	672
Asp His Asp Asp Asp Asp Asn Asp His Thr Asp Asp Asp Tyr Asp Asp	
210 215 220	
gtt tac gac cgc aat ata ggc tct gat gat gat ggt tat gat gcc gat	720
Val Tyr Asp Arg Asn Ile Gly Ser Asp Asp Asp Gly Tyr Asp Ala Asp	
225 230 235 240	
gat gat cga cga tgatcaattt ggactagact tcgttattgg aagggtccga	772
Asp Asp Arg Arg	
tcatcatgcc agtctaatta caaagagaca agaaataaaa atgatgatca aaaaaagaag	832
tcaatccata tacgtaattt tcattgcaat atcaattttg aggtgttttta ttattggcct	892
gtaataatag ttttatttaa taatagcact atagatctca tcctaaccctt tacttattgg	952
gcttatgcgc tgtatgtcca ataaccaagt ttaattttt tcatttttgc atgattactg	1012
caaaaaaaaaa aaaaaaaaaa	1032

<210> 62  
 <211> 244  
 <212> PRT  
 <213> Salsola komarovii

<400> 62	
Pro Gln Arg Arg Pro Asp Pro Val Pro Asn Leu His Gly Gln Leu Phe	
1 5 10 15	
Gln His Arg Asn Pro His His Arg Asp Leu His Pro Cys Arg Ser Pro	
20 25 30	
Ala Met Gly Pro Leu Pro Pro Gln Thr His Leu Arg Trp Tyr Ser Leu	
35 40 45	

Ser Arg Tyr Ser Pro Val Ile Gly Leu Gly Val Gln Trp Lys Pro Ser  
 50 55 60  
 Ser Thr Ser Ala Ala Thr Leu Gln Leu Ser Ile Asp Lys Lys Cys Leu  
 65 70 75 80  
 Ile Phe Gln Leu Ser His Ser Pro Ala Ile Pro Ala Thr Leu Arg Asp  
 85 90 95  
 Leu Leu Leu Asp Asp Arg Val Thr Phe Phe Gly Val His Asn Gly Arg  
 100 105 110  
 Ala Arg Asp Leu Leu Gln Gly Ser His His Glu Leu Asp Val Asn Asn  
 115 120 125  
 Leu Val Asp Leu Ala Glu Glu Asn Gly His Tyr Leu Lys Trp Ser  
 130 135 140  
 Met Glu Asp Met Ala Glu Asp Val Leu Gly Phe Cys Gly Val His Lys  
 145 150 155 160  
 Pro Arg Lys Val Met Leu Ser Gly Trp Asp Gln Tyr Cys Leu Ser Asn  
 165 170 175  
 Asp Gln Val Gln Tyr Ala Cys Val Asp Ala Tyr Val Ser Leu Arg Leu  
 180 185 190  
 Ala Arg Ala Tyr Gly Tyr His Arg Leu Asp His Asp Asp Asp Tyr Asp  
 195 200 205  
 Asp His Asp Asp Asp Asp Asn Asp His Thr Asp Asp Asp Tyr Asp Asp  
 210 215 220  
 Val Tyr Asp Arg Asn Ile Gly Ser Asp Asp Asp Gly Tyr Asp Ala Asp  
 225 230 235 240  
 Asp Asp Arg Arg

<210> 63  
 <211> 1029  
 <212> DNA  
 <213> *Mesembryanthemum crystallinum*  
 <220>  
 <221> CDS  
 <222> (3)...(824)  
 <400> 63  
 ca cat atc agc cac atc cac tta att ccc cac agt ctt agt ctc tta 47  
 His Ile Ser His Ile His Leu Ile Pro His Ser Leu Ser Leu Leu  
 1 5 10 15  
 gac acc cat ctt agt ctt aag cct ctc atg gcc acc gcg gta ttc tca 95

Asp Thr His Leu Ser Leu Lys Pro Leu Met Ala Thr Ala Val Phe Ser			
20	25	30	
cct tct gcc ctt cta tcc acc tcc aca tcc acc tca aca acc cct ctt			143
Pro Ser Ala Leu Leu Ser Thr Ser Thr Ser Thr Thr Pro Leu			
35	40	45	
aaa gct ccc ccc ttg gcc tta acc aag acc cac gta acg atc cca tca			191
Lys Ala Pro Pro Leu Ala Leu Thr Lys Thr His Val Thr Ile Pro Ser			
50	55	60	
tca tca aag cca ccc cta acc aat tta act acc agt tta act gct gtc			239
Ser Ser Lys Pro Pro Leu Thr Asn Leu Thr Thr Ser Leu Thr Ala Val			
65	70	75	
gcc aca gct gct gcc ata atc ctg tcc aca acc cct cca tcg ttt gct			287
Ala Thr Ala Ala Ala Ile Ile Leu Ser Thr Thr Pro Pro Ser Phe Ala			
80	85	90	95
gat gat ttg cag aca aat gca tac aac att tac tac ggc act gct gca			335
Asp Asp Leu Gln Thr Asn Ala Tyr Asn Ile Tyr Tyr Gly Thr Ala Ala			
100	105	110	
agt gca gcc aat tat gga ggc tac ggt ggc aat tcg aac aag aaa gat			383
Ser Ala Ala Asn Tyr Gly Gly Tyr Gly Asn Ser Asn Lys Lys Asp			
115	120	125	
tca gct gag tac ata tat gac gtc cct gca ggt tgg aaa gag aga cta			431
Ser Ala Glu Tyr Ile Tyr Asp Val Pro Ala Gly Trp Lys Glu Arg Leu			
130	135	140	
gta tca aaa gtt gag aag ggt acc aat gga aca gat agt gag ttc ttc			479
Val Ser Lys Val Glu Lys Gly Thr Asn Gly Thr Asp Ser Glu Phe Phe			
145	150	155	
aac ccc aag aag aag aca gag cga gag tac ctt acc tac ctt gct ggt			527
Asn Pro Lys Lys Lys Thr Glu Arg Glu Tyr Leu Thr Tyr Leu Ala Gly			
160	165	170	175
att agg caa cta ggt ccc aaa gaa gtg atc ctc aac aac tta gca ctc			575
Ile Arg Gln Leu Gly Pro Lys Glu Val Ile Leu Asn Asn Leu Ala Leu			
180	185	190	
tca gat gtg aac ctg caa gat caa att tcc agt gca gac tct gtg aca			623
Ser Asp Val Asn Leu Gln Asp Gln Ile Ser Ser Ala Asp Ser Val Thr			
195	200	205	
tca gaa gag agg aaa gat gac aag gga cag gtt tac tat gat tat gag			671
Ser Glu Glu Arg Lys Asp Asp Lys Gly Gln Val Tyr Tyr Asp Tyr Glu			
210	215	220	
att gct gga gct ggt tca cac agt ttg ata tcg gta aca tgt gcc agg			719
Ile Ala Gly Ala Gly Ser His Ser Leu Ile Ser Val Thr Cys Ala Arg			
225	230	235	
aac aag cta tat gcg cat ttt gtt agc gca cca aca ccc gaa tgg aat			767
Asn Lys Leu Tyr Ala His Phe Val Ser Ala Pro Thr Pro Glu Trp Asn			

240	245	250	255	
cgg gat caa gat atg ctg agg cac atc cac aac tca ttt aca aca gtc				815
Arg Asp Gln Asp Met Leu Arg His Ile His Asn Ser Phe Thr Thr Val				
260	265	270		
ggg tca ttc tagaaagtgt atatgataat catttataga gatgtcagag				864
Gly Ser Phe				
aggcatacat ttgaatgtac ttctgatgag ctggacttct tgatctatgt aacattgtaa				924
cgaaaattct ttctgggtta tcagaaacct agtgagtgct tgaaacttgc aatgagaaac				984
tcttcaataa acaatgactt gtatcaaaaa aaaaaaaaaa aaaaa				1029
<210> 64				
<211> 274				
<212> PRT				
<213> <i>Mesembryanthemum crystallinum</i>				
<400> 64				
His Ile Ser His Ile His Leu Ile Pro His Ser Leu Ser Leu Leu Asp				
1	5	10	15	
Thr His Leu Ser Leu Lys Pro Leu Met Ala Thr Ala Val Phe Ser Pro				
20	25	30		
Ser Ala Leu Leu Ser Thr Ser Thr Ser Thr Thr Pro Leu Lys				
35	40	45		
Ala Pro Pro Leu Ala Leu Thr Lys Thr His Val Thr Ile Pro Ser Ser				
50	55	60		
Ser Lys Pro Pro Leu Thr Asn Leu Thr Thr Ser Leu Thr Ala Val Ala				
65	70	75	80	
Thr Ala Ala Ala Ile Ile Leu Ser Thr Thr Pro Pro Ser Phe Ala Asp				
85	90	95		
Asp Leu Gln Thr Asn Ala Tyr Asn Ile Tyr Tyr Gly Thr Ala Ala Ser				
100	105	110		
Ala Ala Asn Tyr Gly Gly Tyr Gly Asn Ser Asn Lys Lys Asp Ser				
115	120	125		
Ala Glu Tyr Ile Tyr Asp Val Pro Ala Gly Trp Lys Glu Arg Leu Val				
130	135	140		
Ser Lys Val Glu Lys Gly Thr Asn Gly Thr Asp Ser Glu Phe Phe Asn				
145	150	155	160	
Pro Lys Lys Lys Thr Glu Arg Glu Tyr Leu Thr Tyr Leu Ala Gly Ile				
165	170	175		
Arg Gln Leu Gly Pro Lys Glu Val Ile Leu Asn Asn Leu Ala Leu Ser				
180	185	190		

Asp Val Asn Leu Gln Asp Gln Ile Ser Ser Ala Asp Ser Val Thr Ser  
195 200 205

Glu Glu Arg Lys Asp Asp Lys Gly Gln Val Tyr Tyr Asp Tyr Glu Ile  
210 215 220

Ala Gly Ala Gly Ser His Ser Leu Ile Ser Val Thr Cys Ala Arg Asn  
225 230 235 240

Lys Leu Tyr Ala His Phe Val Ser Ala Pro Thr Pro Glu Trp Asn Arg  
245 250 255

Asp Gln Asp Met Leu Arg His Ile His Asn Ser Phe Thr Thr Val Gly  
260 265 270

Ser Phe

<210> 65

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 65

gctctgagaa ccgtctagac ttagatgaag gtg

33

<210> 66

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 66

tctctcggttc atctcgagct attacagctc

30

, P

, U, Q<sup>□</sup>^, X, P